

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: <u>12/23</u>	Search Site	Vendors
Searcher: <u>P. S. L. H. E. B. - 308-42.92</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: <u>7</u>	<input checked="" type="checkbox"/> CM-1 <u>6403</u>	<input type="checkbox"/> STN
Elapsed time: <u>17</u>	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: _____	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<u>10</u> <input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: _____	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>Compu</u>

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 9.12597 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-2
Perfect score: 101
Sequence: 1 WIDPENGDSGYAPKFGQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	101	100.0	17	AA197230	Complementary dete
2	101	100.0	17	AAU74407	Heavy chain comple
3	101	100.0	117	AA197235	Variable heavy cha
4	101	100.0	117	AAU74412	Antigen-binding pr
5	101	100.0	240	AAU74419	Antigen-binding pr
6	94	93.1	17	AAE13138	Humanised antibody
7	94	93.1	17	AA197204	VEGF antagonist an
8	94	93.1	17	AAU74416	Heavy chain comple
9	94	93.1	117	AAE13143	Humanised antibody
10	94	93.1	117	AA197209	VEGF antagonist an

11	94	93.1	117	23	AAU74417	Antigen-binding pr
12	94	93.1	136	22	AAE13145	Chimeric p1C11 hea
13	94	93.1	136	22	AA197201	VEGF antagonist an
14	94	93.1	238	23	AAU74420	Antigen-binding pr
15	90	89.1	17	20	AAW89162	Anti-p53 monoclonal
16	90	89.1	20	21	AA1970794	Murine anti-p53 PA
17	90	89.1	112	20	AAW89173	Anti-p53 monoclonal
18	90	89.1	116	21	AA1970787	Murine anti-p53 mo
19	90	89.1	122	20	AA1973531	Humanised Murine C
20	90	89.1	124	15	AA1960565	Anti-carcinoembryo
21	90	89.1	124	15	AA1960566	Anti-carcinoembryo
22	90	89.1	124	20	AA1973528	Murine COL1 VH cha
23	90	89.1	124	20	AA1973530	Humanised Murine C
24	90	89.1	124	20	AA1973536	Humanised Murine C
25	90	89.1	124	20	AA1973537	Humanised Murine C
26	90	89.1	124	20	AA1973538	Humanised Murine C
27	90	89.1	124	20	AA1973539	Humanised Murine C
28	90	89.1	124	20	AA1973540	Humanised Murine C
29	90	89.1	124	20	AA1973541	Humanised Murine C
30	90	89.1	124	20	AA1973542	Humanised Murine C
31	90	89.1	124	20	AA1973543	Humanised Murine C
32	90	89.1	124	23	AAU76632	Murine Col-1(CEA a
33	90	89.1	124	23	AAU76634	Humanised COL-1(CE
34	90	89.1	124	23	AAU76635	Humanised COL-1(CE
35	90	89.1	124	23	AAU76636	Humanised COL-1(CE
36	90	89.1	124	23	AAU76637	Humanised COL-1(CE
37	90	89.1	124	23	AAU76638	Humanised COL-1(CE
38	90	89.1	124	23	AAU76639	Humanised COL-1(CE
39	90	89.1	124	23	AAU76640	Humanised COL-1(CE
40	90	89.1	124	23	AAU76641	Humanised COL-1(CE
41	90	89.1	124	23	AAU76642	Humanised COL-1(CE
42	90	89.1	124	23	AAU76643	Humanised COL-1(CE
43	90	89.1	124	23	AAU76650	Protein template u
44	90	89.1	243	19	AAW60769	Single chain antib
45	90	89.1	270	16	AA1975719	MFE-23 antibody.

ALIGNMENTS

RESULT 1
AA197230
ID AA197230 standard; Protein; 17 AA.
XX
AA197230;
XX
DT 19-DEC-2000 (first entry)
XX
DE Complementary determining region (CDRH2) of anti-SI(KDR) antibody.
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Karposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;

XX WPI; 2000-505966/45.
DR N-PSDB; AAA53762.
XX Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 3; Page 50; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 101; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | | |
Db 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | | |
RESULT 2
AAU74407
ID AAU74407 standard; peptide; 17 AA.
XX
AC AAU74407;
XX
DT 26-MAR-2002 (first entry)
XX
DE Heavy chain complementarity determining region H2 (CDRH2) version #1.
XX
KW Complementarity determining region; CDR; CDRH2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody; heavy chain variable domain.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20278.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX

PS Claim 55; Page 56; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the heavy chain variable domain
CC complementarity determining region H2 (CDRH2) version #1 incorporated
CC into an antigen-binding protein described in the method of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 101; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | | |
Db 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | | |
RESULT 3
AAU97235
ID AAU97235 standard; Protein; 117 AA.
XX
AC AAU97235;
XX
DT 19-DEC-2000 (first entry)
XX
DE Variable heavy chain fragment of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;
XX
DR WPI; 2000-505966/45.
DR N-PSDB; AAA53767.
XX

PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 4; Page 50-51; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 21; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDSGYAPKFG 66

RESULT 4
AAU74412
ID AAU74412 standard; peptide; 117 AA.
XX
AC AAU74412;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein heavy chain variable domain (VH) #1.
XX
KW Antigen-binding protein; antibody heavy chain variable domain;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20283.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 57; Page 57; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; blocking interaction of a protein and
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDSGYAPKFG 66

RESULT 5
AAU74419
ID AAU74419 standard; Protein; 240 AA.
XX
AC AAU74419;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #1.
XX
KW Antigen-binding protein; single chain variable fragment; scFv; antigen;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"
FT 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX
XX
XX
XX
DR WPI; 2002-006189/14;
XX
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
XX
PS Claim 63; Page 62; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an Igg molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
XX invention;
XX
SQ Sequence 240 AA;
Query Match 100.0%; Score 101; DB 23; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFQ 17
|||||
DB 50 WIDPENGDSGYAPKFQ 66
RESULT 6
AAE13138
ID AAE13138 standard; peptide; 17 AA.
XX
AC AAE13138;
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody murine heavy chain hypervariable region (VH) CDR2.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain hypervariable region; VH; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
XX
OS Mus sp.
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10504.
PF
PR 31-MAR-2000; 2000US-0540770.
XX

(IMCL-) IMCLONE SYSTEMS INC.
(CORR) CORNELL RES FOUND INC.
Witte L, Rafii S;
WPI; 2001-662942/76.
N-PSDB; AAD21664.
Inhibiting growth of non-solid tumor cells useful to treat bone marrow
tumors such as leukemias or multiple myeloma comprises treatment with
an antagonist of a vascular endothelial growth factor receptor -
Claim 8; Page 14; 68pp; English.
The invention relates to a method for inhibiting the growth of non-solid
tumour cells that are stimulated by a ligand of vascular endothelial
growth factor receptor (VEGFR) in mammals particularly humans. The method
involves treating the mammals with humanised VEGFR monoclonal antibodies
(antagonists). Humanised monoclonal antibody comprises humanised mouse
variable region joined to human constant region, where the humanised
mouse variable region contains mouse complementarity determining region
(CDR) grafted into human variable region. The method is useful for
treating leukaemias such as acute or chronic myelocytic leukaemia, acute
or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
multiple myelomas and lymphoid cells, particularly those related to
non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
antibody murine heavy chain hypervariable region (VH) CDR-2 used in the
exemplification of the invention.
Sequence 17 AA;
Query Match 93.1%; Score 94; DB 22; Length 17;
Best Local Similarity 94.1%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFQ 17
|||||
DB 1 WIDPENGDSGYAPKFQ 17
RESULT 7
AAB82704
ID AAB82704 standard; Peptide; 17 AA.
XX
AC AAB82704;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 VH CDR-2.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
KW complementarity determining region.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
XX 31-MAR-2000; 2000US-0539692.
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX

DR WPI; 2001-662942/76.
DR N-PSDB; AAD21669.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 15; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain frgament used in the exemplification of the
XX invention.
SQ Sequence 117 AA;
Query Match 93.1%; Score 94; DB 22; Length 117;
Best Local Similarity 94.1%; Pred. No. 8e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 50 WIDPENGSDYAPKFQ 66
RESULT 10
AAB82709
ID AAB82709 standard; Protein; 117 AA.
XX
AC AAB82709;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 26..35
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 99..106
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.

PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26405.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
PS Disclosure; Page 38; 42pp; English.
XX
CC The present sequence is that of the heavy chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 117 AA;
Query Match 93.1%; Score 94; DB 22; Length 117;
Best Local Similarity 94.1%; Pred. No. 8e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 50 WIDPENGSDYAPKFQ 66
RESULT 11
AAU74417
ID AAU74417 standard; peptide; 117 AA.
XX
AC AAU74417;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein heavy chain variable domain (VH) #2.
XX
KW Antigen-binding protein; antibody heavy chain variable domain;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX

PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20288.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 61; Page 60; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; blocking interaction of a protein and
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an Igg molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 117 AA;

Query Match 93.1%; Score 94; DB 23; Length 117;
Best Local Similarity 94.1%; Pred. No. 8e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 50 WIDPENGDSGYAPKFG 66

RESULT 12
AAE13145
ID AAE13145 standard; Protein; 136 AA.
XX
AC AAE13145;
XX
DT 28-JAN-2002 (first entry)
XX
DE Chimeric p1c11 heavy chain fragment.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human; p1c11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader_peptide
FT Protein 20..136
FT /note= "Mature chimeric p1c11 heavy chain fragment"
FT Region 45..54
FT /label= CDR_H1

FT Region 69..85
FT /label= CDR_H2
FT Misc-difference 84
FT /note= "Residue 'O' is present at this location in the
FT sequence shown in fig-11 of the specification"
FT Misc-difference 101
FT /note= "Residue 'O' is present at this location in the
FT sequence shown in fig-11 of the specification"
FT Region 119..125
FT /label= CDR_H3
XX
XX WO200174296-A2.
PN
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10504.
XX
XX 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
PI Witte L, Rafii S;
XX
XX WPI; 2001-662942/76.
DR N-PSDB; AAD21682.
XX
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
XX Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1c11 heavy chain fragment which is used for the construction of chimeric
CC p1c11 IgG expression vector. Chimeric p1c11 heavy chain contains cloned
CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
CC domain (CH).
XX
SQ Sequence 136 AA;

Query Match 93.1%; Score 94; DB 22; Length 136;
Best Local Similarity 94.1%; Pred. No. 9.4e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 69 WIDPENGDSGYAPKFG 85

RESULT 13
AAB82701
ID AAB82701 standard; Protein; 136 AA.
XX
XX AAB82701;
AC
XX 15-OCT-2001 (first entry)
DT
XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.
DE
XX VEGF antagonist antibody; mouse; human; antagonist; VEGF;
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;

KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX

OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..136
FT /label= Mature_protein
FT Region 45..54
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 59..85
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 118..125
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX

PN WO200154723-A1.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US02839.

XX 28-JAN-2000; 2000US-0178791.

PR 31-MAR-2000; 2000US-0539692.

XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.

PA (IMCL-) IMCLONE SYSTEMS INC.

XX Kerbel R.

PI WPI; 2001-514531/56.

XX N-PSDB; AAH26413.

DR Treating or controlling an angiogenic dependent condition (e.g. a
XX neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent
XX

PS Disclosure; Fig 1; 42pp; English.

XX The present sequence is that of the heavy chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX Sequence 136 AA;

Query Match 93.1%; Score 94; DB 22; Length 136;
Best Local Similarity 94.1%; Pred. NO. 9.4e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 69 WIDPENGDSGYAPKFG 85

RESULT 14
ID AAU74420 standard; Protein; 238 AA.
XX
AC AAU74420;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #2.
XX
KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW cytotstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 61"
FT Region 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable fragment
FT protein. Encoded by AAS20285"
FT Region 133..238
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 61"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 63; Page 62-63; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; blocking interaction of a protein and
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
CC invention.
XX

SQ Sequence 238 AA;

Query Match 93.1%; Score 94; DB 23; Length 238;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||||
Db 50 WIDPENGSDYAPKFG 66

RESULT 15

AAW89162

ID AAW89162 standard; peptide; 17 AA.

XX

AC AAW89162;

XX

DT 25-MAR-1999 (first entry)

XX

DE Anti-p53 monoclonal antibody 421 CDR2 heavy chain based peptide.

XX

KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;

KW immune response; tumour associated antigen; metastatic cancer.

XX

OS Mus sp.

OS Synthetic.

XX

PN W09856416-A1.

XX

PD 17-DEC-1998.

XX

PF 09-JUN-1998; 98WO-IL00266.

XX

PR 09-JUN-1997; 97IL-0121041.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;

PI Wolkowicz R;

XX

DR WPI; 1999-070296/06.

XX

PT Use of a monoclonal antibody to a tumour-associated antigen - to

PT induce anti-tumour immunity or elicit an increased immune response

PT to the antigen

XX

PS Claim 7; Page 29; 47pp; English.

XX

CC The present invention describes the use of an immunogen (A) to induce

CC anti-tumour immunity; to elicit an increased immune response to tumour

CC associated antigen (TAA) and/or to induce an immune response to mutant

CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody

CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR

CC (complementarity determining region) on the heavy or light chain of Mab

CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the

CC variable (V) region of Mab, in a gene delivery vehicle. The present

CC sequence represents a peptide based on CDR2 of the heavy chain of

CC anti-p53 Mab 421. Also described is a method for generating sequence-

CC specific, anti-DNA antibodies (Ab) by immunising a mammal with a Mab

CC directed to a domain containing a DNA-binding site of a DNA-binding

CC protein. (A) is used to treat a wide variety of primary and metastatic

CC cancers, particularly those where p53 is involved. Ab are used for

CC diagnosis (e.g to determine critical sequences in animal or plant

CC breeding); to identify bacteria and other parasites; to determine

CC parentage; in forensic science; to isolate specific genes for DNA
CC vaccination; in gene sequencing and cloning; also possibly for activation
CC of selected therapeutic genes in plants, animals and humans. (A) induce
CC an effective anti-tumour response without causing harm to the patient.
CC The method uses (A) to generate anti-TAA by exploiting the anti-idiotypic
CC network.

XX Sequence 17 AA;

Query Match 89.1%; Score 90; DB 20; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||||
Db 1 WIDPENGDTYAPKFG 17

Search completed: December 23, 2002, 07:25:03
Job time : 10.126 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 3.06395 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-2
Perfect score: 101
Sequence: 1 WIDPENGDSGYAPKFG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	90	89.1	124	1	US-08-017-570-4	Sequence 4, Appli
2	90	89.1	124	1	US-08-017-570-6	Sequence 6, Appli
3	90	89.1	124	1	US-08-471-426-4	Sequence 4, Appli
4	90	89.1	124	1	US-08-471-426-6	Sequence 6, Appli
5	90	89.1	124	4	US-09-672-609-1	Sequence 1, Appli
6	90	89.1	124	4	US-09-672-609-3	Sequence 3, Appli
7	90	89.1	124	4	US-09-672-609-4	Sequence 4, Appli
8	90	89.1	124	4	US-09-672-609-5	Sequence 5, Appli
9	90	89.1	124	4	US-09-672-609-6	Sequence 6, Appli
10	90	89.1	124	4	US-09-672-609-7	Sequence 7, Appli
11	90	89.1	124	4	US-09-672-609-8	Sequence 8, Appli
12	90	89.1	124	4	US-09-672-609-9	Sequence 9, Appli
13	90	89.1	124	4	US-09-672-609-10	Sequence 10, Appli
14	90	89.1	124	4	US-09-672-609-11	Sequence 11, Appli
15	90	89.1	124	4	US-09-672-609-12	Sequence 12, Appli
16	90	89.1	124	4	US-09-025-403A-1	Sequence 1, Appli
17	90	89.1	124	4	US-09-025-403A-3	Sequence 3, Appli
18	90	89.1	124	4	US-09-025-403A-4	Sequence 4, Appli
19	90	89.1	124	4	US-09-025-403A-5	Sequence 5, Appli
20	90	89.1	124	4	US-09-025-403A-6	Sequence 6, Appli
21	90	89.1	124	4	US-09-025-403A-7	Sequence 7, Appli
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23	90	89.1	124	4	US-09-025-403A-9	Sequence 9, Appli
24	90	89.1	124	4	US-09-025-403A-10	Sequence 10, Appli
25	90	89.1	124	4	US-09-025-403A-11	Sequence 11, Appli
26	90	89.1	124	4	US-09-025-403A-12	Sequence 12, Appli
27	90	89.1	124	5	PCT-US94-01709-4	Sequence 4, Appli

28	90	89.1	124	5	PCT-US94-01709-6	Sequence 6, Appli
29	90	89.1	270	2	US-08-652-507-2	Sequence 2, Appli
30	90	89.1	535	4	US-08-983-035A-38	Sequence 38, Appli
31	90	89.1	553	2	US-08-661-052-16	Sequence 16, Appli
32	90	89.1	553	4	US-09-188-082-16	Sequence 16, Appli
33	90	89.1	553	4	US-09-364-088-16	Sequence 16, Appli
34	90	89.1	553	4	US-09-102-716-16	Sequence 16, Appli
35	86	85.1	17	4	US-09-171-945-31	Sequence 31, Appli
36	86	85.1	120	4	US-09-171-945-11	Sequence 11, Appli
37	86	85.1	120	4	US-09-171-945-55	Sequence 55, Appli
38	86	85.1	120	4	US-09-171-945-75	Sequence 75, Appli
39	86	85.1	120	4	US-09-171-945-79	Sequence 79, Appli
40	86	85.1	120	4	US-09-171-945-81	Sequence 81, Appli
41	86	85.1	120	4	US-09-171-945-85	Sequence 85, Appli
42	86	85.1	120	4	US-09-171-945-89	Sequence 89, Appli
43	86	85.1	120	4	US-09-171-945-91	Sequence 91, Appli
44	86	85.1	255	4	US-09-171-945-19	Sequence 19, Appli
45	86	85.1	255	4	US-09-171-945-57	Sequence 57, Appli

ALIGNMENTS

RESULT 1
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-4

Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFG 17
|||||||: |||||
DB 50 WIDPENGDTYAPKFG 66

RESULT 2

US-08-017-570-6
; Sequence 6, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-6

Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQG 17

|||||:|||||

Db 50 WIDPENGDTYAPKFQG 66

RESULT 3

US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US

; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4

Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQG 17

|||||:|||||

Db 50 WIDPENGDTYAPKFQG 66

RESULT 4

US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
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Db 50 WIDPENGDTYAPKFG 66

RESULT 5

US-09-672-609-1
; Sequence 1, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-672-609-1

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 6

US-09-672-609-3
; Sequence 3, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3

; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-3

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 7

US-09-672-609-4
; Sequence 4, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 4
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-4

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 8

US-09-672-609-5
; Sequence 5, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-672-609-5

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||: |||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 9
US-09-672-609-6
; Sequence 6, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 6
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
US-09-672-609-6

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||: |||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 10
US-09-672-609-7
; Sequence 7, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.

; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
US-09-672-609-7

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||: |||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 11
US-09-672-609-8
; Sequence 8, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 8
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHATAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
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Db 50 WIDPENGDTYAPKFG 66

RESULT 12
US-09-672-609-9
; Sequence 9, Application US/09672609
; Patent No. 6333405


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; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 9
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHASTAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
; OTHER INFORMATION: Thr-98
; US-09-672-609-9

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Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 WIDPENGDSGYAPKFQG 17
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 Db 50 WIDPENGDTYAPKFQG 66

RESULT 13
 US-09-672-609-10
 ; Sequence 10, Application US/09672609
 ; Patent No. 6333405
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, W.H. Kerr
 ; APPLICANT: Tempest, Philip R.
 ; APPLICANT: Carr, Frank J.
 ; APPLICANT: Harris, William J.
 ; APPLICANT: Armour, Kathryn
 ; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/672,609
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/025,403
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Microsoft Word 97 SR-2
 ; SEQ ID NO 10
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Humanized COL-1 VH, HuVHT
 ; LOCATION: 1..124
 ; OTHER INFORMATION: Humanized heavy chain variable region containing human
 ; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
 ; OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
 US-09-672-609-10

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Qy      1 WIDPENGDSGYAPKFG 17
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Db      50 WIDPENGDTYAPKFG 66

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RESULT 14
 US-09-672-609-11
 ; Sequence 11, Application US/09672609
 ; Patent No. 6333405
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, W.H. Kerr
 ; APPLICANT: Tempest, Philip R.
 ; APPLICANT: Carr, Frank J.
 ; APPLICANT: Harris, William J.
 ; APPLICANT: Armour, Kathryn
 ; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/672,609
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/025,403
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Microsoft Word 97 SR-2
 ; SEQ ID NO 11
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Humanized COL-1 VH, HuVHS
 ; LOCATION: 1..124
 ; OTHER INFORMATION: Humanized heavy chain variable region containing human
 ; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
 ; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
 US-09-672-609-11

Query Match	89.1%;	Score 90;	DB 4;	Length 124;
Best Local Similarity	88.2%;	Pred. No. 4e-07;		
Matches 15;	Conservative	1;	Mismatches 1;	Indels 0; Gaps 0;

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QY      1 WIDPENGDSGYAPKFQG 17
        |||||: |||||
Db     50 WIDPENGDTYAPKFQG 66

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RESULT 15
 US-09-672-609-12
 ; Sequence 12, Application US/09672609
 ; Patent No. 6333405
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, W.H. Kerr
 ; APPLICANT: Tempest, Philip R.
 ; APPLICANT: Carr, Frank J.
 ; APPLICANT: Harris, William J.
 ; APPLICANT: Armour, Kathryn
 ; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/672,609
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/025,403
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Microsoft Word 97 SR-2
 ; SEQ ID NO 12
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Humanized COL-1 VH, HuVHSTAY
 ; LOCATION: 1..124
 ; OTHER INFORMATION: Humanized heavy chain variable region expressed from AT
 ; OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL
 ; OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Thr-76, Thr-78, Ala
 ; OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
 US-09-672-609-12

Query Match 89.18; Score 90; DB 4; Length 124;

Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFQG 17
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Db 50 WIDPENGDTYAPKFQG 66

Search completed: December 23, 2002, 07:33:12
Job time : 4.06395 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 1.5814 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-2
Perfect score: 101
Sequence: 1 WIDPENGDSGYAPKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	10	US-09-976-787-2 Sequence 2, Appli
2	101	100.0	17	10	US-09-865-198-2 Sequence 2, Appli
3	101	100.0	117	10	US-09-976-787-7 Sequence 7, Appli
4	101	100.0	117	10	US-09-865-198-7 Sequence 7, Appli
5	101	100.0	240	10	US-09-976-787-28 Sequence 28, Appl
6	101	100.0	240	10	US-09-865-198-27 Sequence 27, Appl
7	94	93.1	17	10	US-09-976-787-22 Sequence 22, Appl
8	94	93.1	17	10	US-09-865-198-21 Sequence 21, Appl
9	94	93.1	117	10	US-09-976-787-23 Sequence 23, Appl
10	94	93.1	117	10	US-09-865-198-22 Sequence 22, Appl
11	94	93.1	238	10	US-09-976-787-29 Sequence 29, Appl
12	94	93.1	238	10	US-09-865-198-28 Sequence 28, Appl
13	90	89.1	124	9	US-09-974-052-1 Sequence 1, Appli
14	90	89.1	124	9	US-09-974-052-3 Sequence 3, Appli
15	90	89.1	124	9	US-09-974-052-4 Sequence 4, Appli
16	90	89.1	124	9	US-09-974-052-5 Sequence 5, Appli
17	90	89.1	124	9	US-09-974-052-6 Sequence 6, Appli
18	90	89.1	124	9	US-09-974-052-7 Sequence 7, Appli
19	90	89.1	124	9	US-09-974-052-8 Sequence 8, Appli

20	89.1	124	9	US-09-974-052-9	Sequence 9, Appli
21	89.1	124	9	US-09-974-052-10	Sequence 10, Appl
22	89.1	124	9	US-09-974-052-11	Sequence 11, Appl
23	89.1	124	9	US-09-974-052-12	Sequence 12, Appl
24	89.1	124	9	US-09-974-051-1	Sequence 1, Appli
25	89.1	124	9	US-09-974-051-3	Sequence 3, Appli
26	89.1	124	9	US-09-974-051-4	Sequence 4, Appli
27	89.1	124	9	US-09-974-051-5	Sequence 5, Appli
28	89.1	124	9	US-09-974-051-6	Sequence 6, Appli
29	89.1	124	9	US-09-974-051-7	Sequence 7, Appli
30	89.1	124	9	US-09-974-051-8	Sequence 8, Appli
31	89.1	124	9	US-09-974-051-9	Sequence 9, Appli
32	89.1	124	9	US-09-974-051-10	Sequence 10, Appl
33	89.1	124	9	US-09-974-051-11	Sequence 11, Appl
34	89.1	124	9	US-09-974-051-12	Sequence 12, Appl
35	86	85.1	17	10	US-09-910-059-31
36	86	85.1	120	10	US-09-910-059-11
37	86	85.1	120	10	US-09-910-059-55
38	86	85.1	120	10	US-09-910-059-75
39	86	85.1	120	10	US-09-910-059-79
40	86	85.1	120	10	US-09-910-059-81
41	86	85.1	120	10	US-09-910-059-85
42	86	85.1	120	10	US-09-910-059-89
43	86	85.1	120	10	US-09-910-059-91
44	86	85.1	255	10	US-09-910-059-19
45	86	85.1	255	10	US-09-910-059-57

ALIGNMENTS

RESULT 1
US-09-976-787-2
; Sequence 2, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-2

Query Match	100.0%	Score 101;	DB 10;	Length 17;
Best Local Similarity	100.0%	Pred. No. 1.5e-09;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	WIDPENGDSGYAPKFQ 17			
Db 1	WIDPENGDSGYAPKFQ 17			
RESULT 2				
US-09-865-198-2				
; Sequence 2, Application US/09865198				
; Patent No. US20020103345A1				
; GENERAL INFORMATION:				
; APPLICANT: Zhu, Zhenping				
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me				
; TITLE OF INVENTION: Production				
; FILE REFERENCE: 11245/47102				
; CURRENT APPLICATION NUMBER: US/09/865,198				

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2

Query Match 100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 1 WIDPENGDSGYAPKFQ 17

RESULT 3

US-09-976-787-7
; Sequence 7, Application US/09976787

; Patent No. US20020064528A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; APPLICANT: Witte, Larry

; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

; FILE REFERENCE: 11245/46505

; CURRENT APPLICATION NUMBER: US/09/976,787

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/493,539

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 7

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-976-787-7

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 50 WIDPENGDSGYAPKFQ 66

RESULT 4

US-09-865-198-7
; Sequence 7, Application US/09865198

; Patent No. US20020103345A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods

; TITLE OF INVENTION: Production

; FILE REFERENCE: 11245/47102

; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: US 60/206,749

; PRIOR FILING DATE: 2000-05-24

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 7

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Mouse

US-09-865-198-7

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 50 WIDPENGDSGYAPKFQ 66

RESULT 5

US-09-976-787-28

; Sequence 28, Application US/09976787

; Patent No. US20020064528A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; APPLICANT: Witte, Larry

; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

; FILE REFERENCE: 11245/46505

; CURRENT APPLICATION NUMBER: US/09/976,787

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/493,539

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 28

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Mouse

US-09-976-787-28

Query Match 100.0%; Score 101; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 50 WIDPENGDSGYAPKFQ 66

RESULT 6

US-09-865-198-27

; Sequence 27, Application US/09865198

; Patent No. US20020103345A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods

; TITLE OF INVENTION: Production

; FILE REFERENCE: 11245/47102

; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: US 60/206,749

; PRIOR FILING DATE: 2000-05-24

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 27

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Mouse

US-09-865-198-27

Query Match 100.0%; Score 101; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQ 17
|||||
Db 50 WIDPENGDSGYAPKFQ 66

RESULT 7

US-09-976-787-22

; Sequence 22, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-22

Query Match 93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 1 WIDPENGSDYAPKFG 17

RESULT 8

US-09-865-198-21
; Sequence 21, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-21

Query Match 93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 1 WIDPENGSDYAPKFG 17

RESULT 9

US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match 93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 50 WIDPENGSDYAPKFG 66

RESULT 10

US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match 93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||||||| |||||
Db 50 WIDPENGSDYAPKFG 66

RESULT 11

US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 93.1%; Score 94; DB 10; Length 238;

Best Local Similarity 94.1%; Pred. No. 2.6e-07; Indels 1; Gaps 0; Mismatches 1; Matches 16; Conservative 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||
Db 50 WIDPENGDSYAPKFG 66

RESULT 12

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 93.1%; Score 94; DB 10; Length 238;
Best Local Similarity 94.1%; Pred. No. 2.6e-07; Indels 1; Gaps 0; Mismatches 0; Matches 16; Conservative 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||
Db 50 WIDPENGDSYAPKFG 66

RESULT 13

US-09-974-052-1
; Sequence 1, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-052-1

Query Match 89.1%; Score 90; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.4e-07; Indels 1; Gaps 0; Mismatches 1; Matches 15; Conservative 1;

QY 1 WIDPENGDSGYAPKFG 17
|||||
Db 50 WIDPENGDEYAPKFG 66

RESULT 14

US-09-974-052-3
; Sequence 3, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-3

Query Match 89.1%; Score 90; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.4e-07; Indels 1; Gaps 0; Mismatches 1; Matches 15; Conservative 1;

QY 1 WIDPENGDSGYAPKFG 17
|||||
Db 50 WIDPENGDEYAPKFG 66

RESULT 15

US-09-974-052-4
; Sequence 4, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 4
; LENGTH: 124
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-4

Query Match 89.1%; Score 90; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFQ 17
|||||||: |||||
Db 50 WIDPENGDTYAPKFQ 66

Search completed: December 23, 2002, 07:58:18
Job time : 2.5814 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 3.36047 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-2
Perfect score: 101
Sequence: 1 WIDPENGDSGYAPKFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	89.1	82	2	A36025	Ig heavy chain V r
2	82	81.2	118	2	S25174	Ig heavy chain V r
3	82	81.2	136	2	S04576	Ig heavy chain pre
4	80	79.2	116	2	S15672	Ig heavy chain V r
5	78	77.2	137	2	S52445	Ig heavy chain V r
6	67	66.3	85	2	E37262	Ig heavy chain V r
7	67	66.3	98	2	S26918	Ig heavy chain V r
8	67	66.3	132	2	S31596	Ig heavy chain V r
9	67	66.3	136	2	S31600	Ig heavy chain V r
10	67	66.3	143	1	E1HUND	Ig heavy chain pre
11	64	63.4	86	2	S54912	Ig heavy chain V r
12	64	63.4	110	2	PH1670	Ig heavy chain V r
13	64	63.4	171	2	S23623	Ig heavy chain V r
14	63	62.4	127	2	S34014	Ig heavy chain V r
15	62	61.4	98	2	S26938	Ig heavy chain V r
16	62	61.4	98	2	S26912	Ig heavy chain V r
17	62	61.4	99	2	D37262	Ig heavy chain V r
18	62	61.4	107	2	PH1013	Ig heavy chain V r
19	62	61.4	108	2	PH1012	Ig heavy chain V r
20	62	61.4	117	2	S31680	Ig heavy chain V r
21	62	61.4	117	2	S18551	Ig heavy chain V r
22	62	61.4	118	2	S36265	Ig heavy chain V r
23	62	61.4	120	2	S03471	Ig heavy chain V-D
24	62	61.4	122	2	S06823	Ig heavy chain V r
25	62	61.4	123	2	D33548	Ig heavy chain V-1
26	62	61.4	123	2	PH1403	Ig heavy chain V r
27	62	61.4	129	2	S46393	Ig heavy chain V r
28	62	61.4	135	2	S49530	anti-Sm antibody V
29	60	59.4	120	2	S03484	Ig heavy chain V-D

30 60 59.4 221 2 S49220 Ig gamma-1 chain -
31 59 58.4 77 2 S46465 Ig heavy chain V r
32 59 58.4 98 2 S26909 Ig heavy chain V r
33 58 57.4 86 2 S29544 Ig heavy chain V r
34 58 57.4 98 2 S26921 Ig heavy chain V r
35 58 57.4 116 2 S24289 Ig gamma chain V r
36 58 57.4 178 2 S29594 Ig gamma chain (WM
37 57 56.4 114 2 PH1667 Ig heavy chain V r
38 57 56.4 118 2 PH1666 Ig heavy chain V r
39 57 56.4 120 2 S31999 Ig heavy chain V r
40 56.5 55.9 98 2 S26911 Ig heavy chain V r
41 56 55.4 115 2 S03482 Ig heavy chain V-D
42 56 55.4 126 2 I44151 Ig heavy chain V r
43 55 54.5 107 2 A27646 Ig heavy chain V r
44 54 53.5 99 2 C37262 Ig heavy chain V r
45 54 53.5 109 2 PH1668 Ig heavy chain V r

ALIGNMENTS

RESULT 1

A36025

Ig heavy chain V region (PR8-1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999

C;Accession: A36025; E36025

R;Caton, A.J.; Koprowski, H.

Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990

A;Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinator
A;Reference number: A36025; MUID:90349634; PMID:1696733

A;Accession: A36025

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-82 <CAT>

A;Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956

A;Note: PR8-1

A;Accession: E36025

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 19-82 <CA2>

A;Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964

A;Note: clone PR8-21

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 90; DB 2; Length 82;
Best Local Similarity 88.2%; Pred. No. 4.4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQG 17

|||||||: |||||

Db 12 WIDPENGDTYAPKFQG 28

RESULT 2

S25174

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C;Accession: S25174; S33133

R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.

Submitted to the EMBL Data Library, July 1992

A;Description: Structure and binding properties of monoclonal antibodies to core hist

A;Reference number: S25174

A;Accession: S25174

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-118 <MON>

A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259

A;Accession: S33133

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-118 <MO2>
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||:::| |||||
Db 50 WIDPENGDTQYASKFG 66

RESULT 3

S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involve
A;Reference number: S04573; MUID:87133856; PMID:3102255
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 136;
Best Local Similarity 82.4%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||:::| |||||
Db 69 WIDPENGDTQYASKFG 85

RESULT 4

S15672
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S15672
R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,
Bio/Technology 9, 266-271, 1991
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi
A;Reference number: S15672; MUID:91337412; PMID:1367535
A;Accession: S15672
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-116 <TEM>
A;Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 80; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 2.4e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||||:::| |||||
Db 50 WIDPENGDTQYAPKFG 66

RESULT 5

S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged
A;Reference number: S52445
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>
Query Match 77.2%; Score 78; DB 2; Length 137;
Best Local Similarity 76.5%; Pred. No. 6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFG 17
|||||:::| |||||
Db 69 WIDPENGTVYDPKFG 85
RESULT 6
E37262
Ig heavy chain V region (6H2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-May-1997
C;Accession: E37262
R;Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: E37262
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-85 <GOS>
A;Cross-references: GB:M57991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
Query Match 66.3%; Score 67; DB 2; Length 85;
Best Local Similarity 75.0%; Pred. No. 0.0019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IDPENGDSGYAPKFG 17
||| |||:::| |||||
Db 29 IDPANGDTRYDPKFG 44
RESULT 7
S26918
Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0022;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFFQG 17

||:| :|:|||| ||||

Db 50 WMNPNSGNTGYAQKFFQG 66

RESULT 8

S31596

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31596

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31596

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <CUI>

A:Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 132;

Best Local Similarity 58.8%; Pred. No. 0.0031;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFFQG 17

||:| :|:|||| ||||

Db 69 WMNPNSGNTGYAQKFFQG 85

RESULT 9

S31600

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31600

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31600

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 136;

Best Local Similarity 58.8%; Pred. No. 0.0032;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFFQG 17

||:| :|:|||| ||||

Db 69 WMNPNSGNTGYAQKFFQG 85

RESULT 10

ElHUND

Ig heavy chain precursor V-I region (Nd) - human (fragments)

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

C:Accession: A93933; A02026

R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982

A:Title: Cloning and sequence determination of the gene for the human immunoglobulin

A:Reference number: A93933; MUID:83065234; PMID:6815656

A:Accession: A93933

A:Molecule type: mRNA

A:Residues: 1-143 <KEN>

R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.

A:Reference number: A94418

A:Contents: annotation; partial sequence

A:Note: this epsilon chain was isolated from a myeloma protein

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglytamic acid

F;1-15/Domain: signal sequence #status predicted <SIG>

F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>

F;30-113/Domain: immunoglobulin homology <IMM>

F;16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi

F;37-111/Disulfide bonds: #status experimental

Query Match 66.3%; Score 67; DB 1; Length 143;

Best Local Similarity 58.8%; Pred. No. 0.0033;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFFQG 17

||:| :|:|||| ||||

Db 65 WINPNSGGTNYAPRFQG 81

RESULT 11

S54912

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000

C:Accession: S54912

R;Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G.

submitted to the EMBL Data Library, November 1992

A:Reference number: S54912

A:Accession: S54912

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <TOM>

A:Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 86;

Best Local Similarity 64.7%; Pred. No. 0.0057;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFFQG 17

||:| :|:|||| ||||

Db 38 WINPGNGSPSYAKKFFQG 54

RESULT 12

PH1670

Ig heavy chain V region (clone 2A12) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1670

R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staph

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1670

A:Molecule type: mRNA

A:Residues: 1-110 <HIL>

A:Experimental source: B cell

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 110;
Best Local Similarity 58.8%; Pred. No. 0.0075;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
::: ||::||| ||||
Db 42 WMNANGNTGYAQKFG 58

RESULT 13

S23623
Ig heavy chain V region precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C;Accession: S23623

R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23623

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-171 <OLE>

A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 171;
Best Local Similarity 58.8%; Pred. No. 0.012;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||:|:| ||||
Db 69 WINPNSGGTGYGQKFG 85

RESULT 14

S34014

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C;Accession: S34014; S30535

R;Marlette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A;Reference number: S34001; MUID:93209281; PMID:7681398

A;Accession: S34014

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-127 <MAR>

A;Cross-references: EMBL:Z18321

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 127;
Best Local Similarity 52.9%; Pred. No. 0.012;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||:|:| ||||
Db 50 WMNPSGNTGYAQKFG 66

RESULT 15

S26938

Ig heavy chain V region (DP-75) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938

R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26938

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-98 <TOM>

A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.4%; Score 62; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.014;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
||:|:| ||||
Db 50 WINPNSGGTNYAQKFG 66

Search completed: December 23, 2002, 07:31:31

Job time : 4.36047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 1.68023 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-2
Perfect score: 101
Sequence: 1 WIDPENGDSGYAPKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	66.3	147	1 HV1C_HUMAN	P01744 homo sapien
2	51	50.5	117	1 HV1B_HUMAN	P01743 homo sapien
3	51	50.5	117	1 HV1G_HUMAN	P23083 homo sapien
4	50	49.5	350	1 NUD9_HUMAN	Q9bw91 homo sapien
5	46	45.5	117	1 HV12_MOUSE	P01756 mus musculu
6	46	45.5	117	1 HV13_MOUSE	P01757 mus musculu
7	46	45.5	118	1 HV51_MOUSE	P06330 mus musculu
8	46	45.5	245	1 VE4_HPV5B	P26550 human papil
9	46	45.5	839	1 GLT5_WHEAT	P10388 triticum ae
10	45	44.6	117	1 HV52_MOUSE	P06327 mus musculu
11	45	44.6	245	1 VE4_HPV05	P06924 human papil
12	44	43.6	101	1 GLT1_WHEAT	P02861 triticum ae
13	44	43.6	474	1 GLN1_FRAAL	P46033 frankia aln
14	43	42.6	132	1 ROMA_KLEPN	Q48412 klebsiella
15	43	42.6	159	1 17KD_RICPR	P16624 rickettsia
16	43	42.6	159	1 17KD_RICTY	P22882 rickettsia
17	43	42.6	238	1 Y1GB_ECOLI	P23306 escherichia
18	43	42.6	524	1 FTWH_MYCTU	O06223 mycobacteri
19	43	42.6	838	1 GLT4_WHEAT	P08489 triticum ae
20	42	41.6	80	1 17KD_RICCA	P29697 rickettsia
21	42	41.6	117	1 HV14_MOUSE	P01758 mus musculu
22	42	41.6	120	1 HV03_MOUSE	P01747 mus musculu
23	42	41.6	154	1 17KD_RICAM	P50927 rickettsia
24	42	41.6	154	1 17KD_RICAU	P50928 rickettsia
25	42	41.6	154	1 17KD_RICMO	P50929 rickettsia
26	42	41.6	154	1 17KD_RICPA	P50930 rickettsia
27	42	41.6	154	1 17KD_RICRH	P50931 rickettsia
28	42	41.6	159	1 17KD_RICCN	P05372 rickettsia
29	42	41.6	159	1 17KD_RICJA	Q52764 rickettsia
30	42	41.6	809	1 CN4D_HUMAN	Q08499 homo sapien
31	42	41.6	4543	1 LRPI_CHICK	P98157 gallus gall
32	41.5	41.1	504	1 AFX1_HUMAN	P98177 homo sapien
33	41.5	41.1	597	1 ETFD_CABEL	Q11190 c probabie

34	41.5	41.1	957	1 AMPE_HUMAN	Q07075 homo sapien
35	41	40.6	140	1 HV02_MOUSE	P01746 mus musculu
36	41	40.6	434	1 ENO_STAAM	Q99vk5 staphylococ
37	41	40.6	434	1 ENO_STAAY	O69174 staphylococ
38	41	40.6	434	1 ENO_STRPY	P82479 streptococc
39	41	40.6	482	1 CALB_RAT	P20909 rattus norv
40	41	40.6	670	1 CUI3_HUMAN	O95447 homo sapien
41	41	40.6	1281	1 IP3S_MOUSE	Q92329 mus musculu
42	41	40.6	1804	1 CALB_MOUSE	Q61245 mus musculu
43	41	40.6	1806	1 CALB_HUMAN	P12107 homo sapien
44	41	40.6	2346	1 COAL_BOVIN	Q9tts3 bos taurus
45	41	40.6	2346	1 COAL_SHEEP	Q28559 ovis aries

ALIGNMENTS

RESULT 1					
HV1C_HUMAN					
ID	HV1C_HUMAN	STANDARD;	PRT;	147 AA.	
AC	P01744;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ig heavy chain V-I region ND precursor (Fragments).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83065234; PubMed=6815656;				
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,				
RA	Bell L.O., Gould H.J.;				
RT	"Cloning and sequence determination of the gene for the human				
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RN	[2]				
RP	SEQUENCE OF 20-147.				
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;				
RL	(In) Bach M.K. (eds.);				
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,				
RL	Marcel Dekker, New York (1978).				
CC	-I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA				
CC	PROTEIN.				
DR	PIR; A02026; ELHUND.				
DR	HSSP; P01789; IMCP.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00406; IGV; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL 1 19				
FT	CHAIN 20 147				
FT	MOD_RES 20 20				
FT	DISULFID 41 115				
FT	CONFLICT 21 21				
FT	CONFLICT 53 54				
FT	CONFLICT 67 68				
FT	CONFLICT 125 125				
FT	NON_TER 147 147				
SQ	SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;				
Query Match 66.3%; Score 67; DB 1; Length 147;					
Best Local Similarity 58.8%; Pred. No. 0.001;					
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;					
QY	1 WIDPENGDSGYAPKFQ 17				
	: : :				
Db	69 WINPNSGGTNYAPRFQ 85				
RESULT 2					


```
DR MIM; 606022; -.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00893; NUDIX; 1.
KW Hydrolase.
FT DOMAIN 215 237 NUDIX BOX.
SQ SEQUENCE 350 AA; 39125 MW; 2EA5B24B88FB3420 CRC64;

Query Match 49.5%; Score 50; DB 1; Length 350;
Best Local Similarity 46.7%; Pred. No. 1.4;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKF 15
| | | : | : | | |
Db 110 WADPQISENFSPKF 124

RESULT 5
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFQ 17
| : | | | : | | | |
Db 51 INPNNGGTSYNQKFKG 66

RESULT 6
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFQ 17
| : | | | : | | | |
Db 51 INPNNGGTSYNQKFKG 66

RESULT 7
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFQ 17
| : | | | : | | | |
Db 51 INPNNGGTSYNQKFKG 66
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```
RESULT 8
VE4_HPVS5B
ID VE4_HPVS5B STANDARD; PRT; 245 AA.
AC P26550;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Probable E4 protein.
OS Human papillomavirus type 5b.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10599;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91306467; PubMed=1649510;
RA Yabe Y., Sakai A., Hitsumoto T., Kato H., Ogura H.;
RT "A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic
RT segment amplified in a carcinoma: nucleotide sequences and genomic
RT organizations."
RL Virology 183:793-798(1991).
CC -----
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CC -----
DR EMBL; D90252; BAA14296.1; -
DR PIR; C40480; W4WLB5.
KW Early protein.
SQ SEQUENCE 245 AA; 25622 MW; E4944F95B3D353B2 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 245;
Best Local Similarity 61.5%; Pred. No. 4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PENGDSGYAPKFQ 16
Db 155 PHNGHSGHGPKVQ 167

RESULT 9
GLT5_WHEAT
ID GLT5_WHEAT STANDARD; PRT; 839 AA.
AC P10388;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glutenin; high molecular weight subunit DX5 precursor.
GN GLU-1D-1B OR GLU-D1-1B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Cheyenne;
RX MEDLINE=89098419; PubMed=2563152;
RA Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.,
RA Malpica-Pomero J.M.;
RT "Nucleotide sequences of the two high-molecular-weight glutenin genes
RT from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
RT Cheyenne."
RL Nucleic Acids Res. 17:461-462(1989).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RC STRAIN=cv. Cheyenne;
RA Anderson O.D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
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CC PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
CC VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
CC -!- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
CC -!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
CC GROUP 1 CHROMOSOMES OF WHEAT.
CC -!- MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE
CC NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQPGQ AND
CC GQPGQGQGGYPTS.
CC -----
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CC -----
DR EMBL; X12928; CAA31395.1; -
DR PIR; S02262; S02262.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
DR PRINTS; PR00210; GLUTENIN.
KW Seed storage protein; Repeat; Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 839 GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
FT DX5.
FT DOMAIN 131 801 REPEATS.
FT SEQUENCE 839 AA; 89359 MW; 0F14E1106D552643 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 839;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
Db 158 WEEPEQGQGGYYP 170

RESULT 10
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments."
RL Cell 40:271-281(1985).
CC -----
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CC -----
DR EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
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KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 44.6%; Score 45; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 2.5;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
|||:|:| |||
Db 69 WIYPGDGSKYNEKFKG 85

RESULT 11
VE4_HPVO5
ID VE4_HPVO5 STANDARD; PRT; 245 AA.
AC P06924;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable E4 protein.
OS Human papillomavirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10578;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87207670; PubMed=3033892;
RA Zachow K.R., Ostrow R.S., Faras A.J.;
RT "Nucleotide sequence and genome organization of human papillomavirus
type 5.";
RL Virology 158:251-254(1987).
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CC -----
CC EMBL; M17463; AAA46987.1; -.
CC PIR; E26277; W4WL5.
KW Early protein.
SQ SEQUENCE 245 AA; 25758 MW; 8F5ECDFB28D87EE0 CRC64;

Query Match 44.6%; Score 45; DB 1; Length 245;
Best Local Similarity 61.5%; Pred. No. 5.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PENGDSGYAPKFKQ 16
||| ||: |||
Db 155 PHNGHSGHEPKVQ 167

RESULT 12
GLT1_WHEAT
ID GLT1_WHEAT STANDARD; PRT; 101 AA.
AC P02861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Glutenin, high molecular weight subunit PC256 (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Forde J., Forde B.G., Fry R.P., Kreis M., Shewry P.R., Miflin B.J.;
RT "Identification of barley and wheat cDNA clones related to the high-
RT M-r polypeptides of wheat gluten.";
RL FEBS Lett. 162:360-366(1983).
CC -!- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
CC PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
CC VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
CC -!- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
CC -!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
CC GROUP 1 CHROMOSOMES OF WHEAT.
CC -----
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CC -----
CC EMBL; X00054; CAA24933.1; -.
CC PIR; A03352; EEWTL.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Seed storage protein; Repeat; Multigene family.
FT NON_TER 1 1
SQ SEQUENCE 101 AA; 10896 MW; EF6D6ADDDFEED993 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 101;
Best Local Similarity 46.2%; Pred. No. 3.1;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
|:| | |||
Db 12 WLQPRQGQGYYP 24

RESULT 13
GLN1_FRAAL
ID GLN1_FRAAL STANDARD; PRT; 474 AA.
AC P46033;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase I)
DE (GSI).
GN GLNA.
OS Frankia alni.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Frankineae; Frankiaceae; Frankia.
OX NCBI_TaxID=1859;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cp11;
RX MEDLINE=93273742; PubMed=8099074;
RA Hosted T.J., Rochefort D.A., Benson D.R.;
RT "Close linkage of genes encoding glutamine synthetases I and II in
RT Frankia alni Cp11.";
RL J. Bacteriol. 175:3679-3684(1993).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
CC L-glutamine.
CC -!- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED
CC BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE
CC (BY SIMILARITY).
CC -!- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGONS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII)
CC CAN BE FOUND IN THIS NITROGEN FIXING BACTERIA, GSI IS A TYPICAL
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CC PROKARYOTIC GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE
CC EUKARYOTIC ENZYME.
CC -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; L10631; -; NOT_ANNOTATED_CDS.
CC HSSP; P06201; ILGR.
CC InterPro; IPR001691; GLN_synth.
CC InterPro; IPR004809; GlnA.
CC InterPro; IPR001637; GlnA_adenyltn.
CC Pfam; PF00120; gln-synt; 1.
CC ProDom; PD001057; GlnA_adenyltn; 1.
CC TIGRFAMS; TIGR00653; GlnA; 1.
CC PROSITE; PS00180; GLNA_1; 1.
CC PROSITE; PS00181; GLNA_ATP; 1.
CC PROSITE; PS00182; GLNA_ADENYLATION; 1.
CC Nitrogen fixation; Ligase; Multigene family.
KW BINDING 402 402 AMP (UNDER CONDITIONS OF ABUNDANT
FT GLUTAMINE) (BY SIMILARITY).
FT SEQUENCE 474 AA; 53951 MW; FE1DB19AC1735652 CRC64;
SQ
Query Match 43.6%; Score 44; DB 1; Length 474;
Best Local Similarity 53.8%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 ENGDSGYAPKFG 17
Db 168 EGGNLEGYKPRFKG 180
RESULT 14
ROMA_KLEPN STANDARD; PRT; 132 AA.
ID ROMA_KLEPN STANDARD; PRT; 132 AA.
AC Q48412;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Outer membrane protein roma (Fragment).
GN ROMA.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECL8;
RX MEDLINE=96032015; PubMed=7551053;
RA George A.M., Hall R.M., Stokes H.W.;
RT "Multidrug resistance in Klebsiella pneumoniae: a novel gene, ramA,
RT confers a multidrug resistance phenotype in Escherichia coli.";
RL Microbiology 141:1909-1920(1995).
CC -!- SIMILARITY: TO M.TUBERCULOSIS RV0906.
CC -----
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CC -----
CC EMBL; U19581; AAA5696.1; -.
CC Outer membrane.
KW NON_TER 1 1
FT SEQUENCE 132 AA; 14745 MW; BCB216F27F9C853B CRC64;
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Query Match 42.6%; Score 43; DB 1; Length 132;
Best Local Similarity 63.6%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 6 NGDSGYAPKFQ 16
Db 44 SGDSGYGPHFK 54
RESULT 15
17KD_RICPR STANDARD; PRT; 159 AA.
ID 17KD_RICPR STANDARD; PRT; 159 AA.
AC P16624;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 17 kDa surface antigen precursor.
GN OMP OR RP833.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=89359171; PubMed=2768201;
RA Anderson B.E., Tzianabos T.;
RT "Comparative sequence analysis of a genus-common rickettsial antigen
RT gene.";
RL J. Bacteriol. 171:5199-5201(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor (Probable).
CC -----
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CC -----
CC EMBL; M28482; AAA26378.1; ALT_SEQ.
CC EMBL; AJ235273; CAA15258.1; -.
CC PIR; D33971; D33971.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
FT SIGNAL 1 19
FT CHAIN 20 159 17 KDA SURFACE ANTIGEN.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
SQ SEQUENCE 159 AA; 16672 MW; A33D404B65EEB071 CRC64;
Query Match 42.6%; Score 43; DB 1; Length 159;
Best Local Similarity 54.5%; Pred. No. 7.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 WIDPENGDSGY 11
Db 102 WRNPDNGNHGY 112
Search completed: December 23, 2002, 07:26:02
Job time : 3.68023 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 7.05039 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-2
Perfect score: 101
Sequence: 1 WIDPENGDSGYAPKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	74.3	468	11	Q99L31	Q99L31 mus musculu
2	58	57.4	614	4	Q96GA6	Q96ga6 homo sapien
3	57	56.4	109	11	Q9JL85	Q9jl85 mus musculu
4	56.5	55.9	150	4	Q9Y298	Q9y298 homo sapien
5	56	55.4	497	4	Q8WY24	Q8wy24 homo sapien
6	55	54.5	125	4	Q9UL95	Q9ul95 homo sapien
7	54	53.5	119	4	Q9UL94	Q9ul94 homo sapien
8	54	53.5	481	11	Q8VCV5	Q8vcv5 mus musculu
9	51	50.5	124	4	Q9UL92	Q9ul92 homo sapien
10	50	49.5	300	11	Q9D0U2	Q9d0u2 mus musculu
11	50	49.5	350	4	Q96KB3	Q96kb3 homo sapien
12	50	49.5	500	4	Q9BRV0	Q9brv0 homo sapien
13	49	48.5	754	10	Q94IL2	Q94il2 secale cere
14	49	48.5	754	10	Q94IK9	Q94ik9 secale cere
15	49	48.5	754	10	Q93WF0	Q93wf0 secale cere
16	48	47.5	311	16	Q92ME3	Q92me3 rhizobium m

17	48	47.5	329	5	Q27501	Q27501 caenorhabdi
18	48	47.5	403	16	Q8Y1U7	Q8ylu7 ralstonia s
19	48	47.5	484	11	Q99LA6	Q99la6 mus musculu
20	48	47.5	526	17	Q8TJE3	Q8tje3 methanosarc
21	47.5	47.0	474	11	Q8R3H6	Q8r3h6 mus musculu
22	47	46.5	102	11	Q9JL79	Q9jl79 mus musculu
23	47	46.5	208	16	Q92F12	Q92f12 listeria in
24	47	46.5	209	16	Q8YA89	Q8ya89 listeria mo
25	47	46.5	366	5	Q27528	Q27528 caenorhabdi
26	47	46.5	375	5	Q9XW33	Q9xw33 caenorhabdi
27	47	46.5	509	17	Q9HMH4	Q9hmh4 halobacteri
28	47	46.5	520	11	Q921T2	Q921t2 mus musculu
29	46	45.5	117	11	Q9QXF0	Q9qxf0 mus musculu
30	46	45.5	117	11	Q9QXE9	Q9qxe9 mus musculu
31	46	45.5	159	4	Q96QS0	Q96qs0 homo sapien
32	46	45.5	327	5	Q23671	Q23671 caenorhabdi
33	46	45.5	363	2	Q93NF9	Q93nf9 arthrobacte
34	46	45.5	390	9	Q9T1R0	Q9t1r0 bacterioph
35	46	45.5	481	11	Q91WT1	Q91wt1 mus musculu
36	46	45.5	626	3	Q99112	Q99112 ustilago ma
37	46	45.5	1737	11	Q9J1O4	Q9ji04 rattus norv
38	45.5	45.0	118	11	Q9Z1C4	Q9z1c4 mus musculu
39	45	44.6	138	2	Q9F8N0	Q9f8n0 carboxydoth
40	45	44.6	168	17	O27394	O27394 methanobact
41	45	44.6	322	5	Q8SQW6	Q8sqw6 encephalito
42	45	44.6	399	2	Q9KX26	Q9kx26 pseudomonas
43	45	44.6	405	16	Q98M10	Q98mi0 rhizobium m
44	45	44.6	638	16	Q92XY6	Q92xy6 rhizobium m
45	45	44.6	697	17	Q8TJQ4	Q8tjq4 methanosarc

ALIGNMENTS

RESULT 1
Q99L31
ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 74.3%; Score 75; DB 11; Length 468;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 WIDPENGDSGYAPKFQ 16
|||||:|:|
Db 69 WIDPEDGETKYAPKFQ 84

```
RESULT 2
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 57.4%; Score 58; DB 4; Length 614;
Best Local Similarity 62.5%; Pred. No. 0.93;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFQ 16
||| |||: |||
Db 69 WITPENGNTNYAQKFQ 84

RESULT 3
Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 56.4%; Score 57; DB 11; Length 109;
Best Local Similarity 68.8%; Pred. No. 0.18;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 IDPENGDSGYAPKFQ 17
||| | | | | | |
Db 43 IDPATGHSKYDPKFQ 58

RESULT 4
Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE IgG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=96577749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor."
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAAL1829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 55.9%; Score 56.5; DB 4; Length 150;
Best Local Similarity 55.0%; Pred. No. 0.31;
Matches 11; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 WI--DPENGDSGYAPKFQ 17
|: |||:| | | | |
Db 66 WVGSEDPESGESIYAREFQ 85

RESULT 5
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SNC66, a Ig-like gene which is
RT down-regulated in colorectal cancer."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 2.
```


RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.",
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 50.5%; Score 51; DB 4; Length 124;
Best Local Similarity 56.2%; Pred. No. 1.8;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFG 17
Db 51 INPSGGSTSYAQKFG 66

RESULT 10
Q9D0U2
ID Q9D0U2 PRELIMINARY; PRT; 300 AA.
AC Q9D0U2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 1190002C07Rik protein.
GN NUDT9 OR 1190002C07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004444; BAB23305.1; -.
DR MGD; MGI:1921417; Nudt9.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
SQ SEQUENCE 300 AA; 33550 MW; 5BD71C72E2A4DA50 CRC64;

Query Match 49.5%; Score 50; DB 11; Length 300;
Best Local Similarity 46.7%; Pred. No. 7.5;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKF 15
Db 60 WADPQISESNFSPKF 74

RESULT 11
Q96KB3
ID Q96KB3 PRELIMINARY; PRT; 350 AA.
AC Q96KB3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA FLJ14389 fis, clone HEMBA1002876.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO, AND MAINLY HEAD;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027295; BAB55021.1; -.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
SQ SEQUENCE 350 AA; 39042 MW; 8BE1A31ECCFB343D CRC64;

Query Match 49.5%; Score 50; DB 4; Length 350;
Best Local Similarity 46.7%; Pred. No. 8.9;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKF 15
Db 110 WADPQISESNFSPKF 124

RESULT 12
Q9BRV0
ID Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 54.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.


```
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match          49.5%; Score 50; DB 4; Length 500;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
   ||| : : | ||||
Db 69 WISPSSDNTFRAKKFG 85

RESULT 13
Q94IL2
ID Q94IL2 PRELIMINARY; PRT; 754 AA.
AC Q94IL2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
   encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
   orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314773; CAC40674.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA; 80179 MW; 89B4D795A3DC91BB CRC64;

Query Match          48.5%; Score 49; DB 10; Length 754;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
   ||| | |||
Db 665 WLQPEQGQEGYYP 677

RESULT 14
Q94IK9
ID Q94IK9 PRELIMINARY; PRT; 754 AA.
AC Q94IK9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
   encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
   encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314778; CAC40670.1; -.
DR EMBL; AJ314778; CAC40679.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 754 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA; 80179 MW; 89B4D795A3DC91BB CRC64;

Query Match          48.5%; Score 49; DB 10; Length 754;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
   ||| | |||
Db 665 WLQPEQGQEGYYP 677

RESULT 14
Q94IK9
ID Q94IK9 PRELIMINARY; PRT; 754 AA.
AC Q94IK9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
   encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
   orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314768; CAC40670.1; -.
DR EMBL; AJ314778; CAC40679.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 754 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA; 80270 MW; 28A1B2D0613082F7 CRC64;

Query Match          48.5%; Score 49; DB 10; Length 754;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
   ||| | |||
Db 665 WLQPEQGQEGYYP 677
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```
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
   encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SMITH;
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
   orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314779; CAC40680.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 754 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA; 80267 MW; 6F160E5F25455FC7 CRC64;

Query Match          48.5%; Score 49; DB 10; Length 754;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
   ||| | |||
Db 665 WLQPEQGQEGYYP 677

RESULT 15
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ID Q93WF0 PRELIMINARY; PRT; 754 AA.
AC Q93WF0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PETKUS;
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
   encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PETKUS;
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
   orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314768; CAC40670.1; -.
DR EMBL; AJ314778; CAC40679.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 754 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA; 80270 MW; 28A1B2D0613082F7 CRC64;

Query Match          48.5%; Score 49; DB 10; Length 754;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
   ||| | |||
Db 665 WLQPEQGQEGYYP 677
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Search completed: December 23, 2002, 07:29:44
Job time : 10.0504 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 4.29457 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	21	AA197231
2	51	100.0	8	22	AAE13139
3	51	100.0	8	22	AA197235
4	51	100.0	8	23	AAU74408
5	51	100.0	117	21	AA197235
6	51	100.0	117	22	AAE13143
7	51	100.0	117	22	AA197235
8	51	100.0	117	23	AAU74412
9	51	100.0	117	23	AAU74417
10	51	100.0	136	22	AAE13145
					Complementary dete
					Humanised antibody
					VEGF antagonist an
					Heavy chain comple
					Variable heavy cha
					Humanised antibody
					VEGF antagonist an
					Antigen-binding pr
					Chimeric pIC11 hea

11	51	100.0	136	22	AA197231	VEGF antagonist an
12	51	100.0	238	23	AAU74420	Antigen-binding pr
13	51	100.0	240	23	AAU74419	Antigen-binding pr
14	39	76.5	11	17	AA197235	VLA-4 binding pept
15	38	74.5	120	12	AA197231	Control fusion pro
16	38	74.5	322	23	AAE15536	Beta vulgaris RNA
17	38	74.5	364	21	AA197235	Arabidopsis thalia
18	38	74.5	364	21	AA197235	Arabidopsis thalia
19	38	74.5	365	21	AA197235	Arabidopsis thalia
20	38	74.5	365	21	AA197235	Arabidopsis thalia
21	38	74.5	387	21	AA197235	Arabidopsis thalia
22	38	74.5	387	21	AA197235	Arabidopsis thalia
23	38	74.5	564	21	AA197235	Arabidopsis thalia
24	38	74.5	738	21	AA197235	Arabidopsis thalia
25	38	74.5	745	21	AA197235	Arabidopsis thalia
26	37	72.5	248	22	AA197235	Drosophila melanog
27	37	72.5	264	20	AA197235	Fragment of human
28	37	72.5	279	22	AA197235	Human protein sequ
29	37	72.5	300	22	AA197235	Drosophila melanog
30	37	72.5	485	22	AA197235	Novel human diagno
31	37	72.5	562	23	AA197235	Neisseria meningit
32	37	72.5	562	23	AA197235	Neisseria meningit
33	37	72.5	562	23	AA197235	Neisseria meningit
34	37	72.5	633	21	AA197235	Human secreted pro
35	36	70.6	97	17	AA197235	Salmonella sero gp
36	36	70.6	191	23	AA197235	Listeria monocytog
37	36	70.6	307	22	AA197235	Drosophila melanog
38	36	70.6	441	23	AA197235	Herbicideally activ
39	36	70.6	525	21	AA197235	Raccoonpox virus B
40	36	70.6	591	12	AA197235	Gamma glutamyl tra
41	36	70.6	624	19	AA197235	Thyroid peroxidase
42	36	70.6	626	19	AA197235	Thyroid peroxidase
43	36	70.6	663	19	AA197235	Thermotoga maritim
44	36	70.6	666	19	AA197235	Thermotoga neapoli
45	36	70.6	680	18	AA197235	Thermotoga maritim

ALIGNMENTS

RESULT 1
AA197231
ID AA197231 standard; Protein; 8 AA.

AC AA197231;
XX
DT 19-DEC-2000 (first entry)
XX

DE Complementary determining region (CDRH3) of anti-SI(KDR) antibody.
XX Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.

OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.

XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;

XX WPI; 2000-505966/45.
DR N-PSDB; AAA53763.
XX Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 3; Page 50; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db |||||
1 YYGDYEGY 8

RESULT 2
AAE13139
ID AAE13139 standard; peptide; 8 AA.
XX
AC AAE13139;
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody murine heavy chain hypervariable region (VH) CDR3.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain hypervariable region; VH; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse;
XX
OS Mus sp.
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafil S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21665.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -

XX Claim 8; Page 14; 68pp; English.
PS
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody murine heavy chain hypervariable region (VH) CDR-3 used in the
CC exemplification of the invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db |||||
1 YYGDYEGY 8

RESULT 3
AAB82705
ID AAB82705 standard; Peptide; 8 AA.
XX
AC AAB82705;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 VH CDR-3.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
KW complementarity determining region.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
PS Disclosure; Page 37; 42pp; English.
XX

CC The present sequence is that of complementarity determining region
CC 3 of the heavy chain variable region (see also AAB82701) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| | | | | | | |
Db 1 YGDIYEGY 8

RESULT 4
AAU74408
ID AAU74408 standard; peptide; 8 AA.
XX
AC AAU74408;
XX
DT 26-MAR-2002 (first entry)
XX
DE Heavy chain complementarity determining region H3 (CDRH3).
XX
KW Complementarity determining region; CDR; CDRH3; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody heavy chain variable domain.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20279.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 55; Page 56; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the heavy chain variable domain
CC complementarity determining region H3 (CDRH3) incorporated into an
CC antigen-binding protein described in the method of the invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| | | | | | | |
Db 1 YGDIYEGY 8

RESULT 5
AAU97235
ID AAU97235 standard; Protein; 117 AA.
XX
AC AAU97235;
XX
DT 19-DEC-2000 (first entry)
XX
DE Variable heavy chain fragment of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;
XX
DR WPI; 2000-505966/45.
DR N-PSDB; AAA53767.
XX
PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 4; Page 50-51; 55pp; English.

XX New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumor cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.

XX SQ Sequence 117 AA;
Query Match 100.0%; Score 51; DB 21; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
Db 99 YGDIYEGY 106
|||||

RESULT 6
AAE13143
ID AAE13143 standard; Protein; 117 AA.
XX
AC AAE13143
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody heavy chain fragment.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytototoxic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
PN WO200174296-A2.
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR-) CORNELL RES FOUND INC.
XX
PI Witte L Rafil S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21669.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 15; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse

CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain fragment used in the exemplification of the
CC invention.

XX SQ Sequence 117 AA;
Query Match 100.0%; Score 51; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
Db 99 YGDIYEGY 106
|||||

RESULT 7
AAB82709
ID AAB82709 standard; Protein; 117 AA.
XX
AC AAB82709;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 26..35
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 99..106
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26405.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -

XX PS Disclosure; Page 38; 42pp; English.

XX CC The present sequence is that of the heavy chain variable region of

CC IMC-1C11, a mouse-human chimeric antibody that has vascular

CC endothelial growth factor (VEGF) antagonist activity. The antibody,

CC or a fragment of it, can be used as an anti-angiogenic molecule,

CC together with a chemotherapeutic acid, for the treatment of an

CC angiogenic dependent condition in a mammal, especially a human.

CC The invention relates generally to a method of treating or

CC controlling an angiogenic dependent condition by administering an

CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a

CC regression or arrest of the condition while minimising or

CC preventing significant toxicity of the chemotherapeutic agent.

CC The anti-angiogenic molecule inhibits or blocks the action of a

CC vascular endothelium survival factor such as VEGF or its receptor,

CC and is especially IMC-1C11. Conditions that can be treated include

CC a neoplasm, a collagen-vascular disease or an autoimmune disease,

CC especially a solid tumour, including breast carcinoma, lung

CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,

CC ovarian carcinoma, neuroblastoma, central nervous system tumour,

CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 22; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8

Db 99 YGDIYEGY 106

RESULT 8

AAU74412

ID AAU74412 standard; peptide; 117 AA.

XX AC AAU74412;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein heavy chain variable domain (VH) #1.

XX KW Antigen-binding protein; antibody heavy chain variable domain;

XX KW cytotstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

XX KW vascular endothelial growth factor receptor; VEGF;

XX KW cell proliferation inhibitor.

XX OS Mus sp.

XX PN WO200190192-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX WPI; 2002-106189/14.

DR N-PSDB; AAS20283.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX Claim 57; Page 57; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

CC light chain constant domain (CL domain), and P2 has an antigen-binding

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC neutralising the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This sequence represents a heavy chain variable domain (VH) incorporated

CC into Fv, an engineered protein containing a heavy chain variable domain

CC and a light chain variable domain in one polypeptide chain, described in

CC the method of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8

Db 99 YGDIYEGY 106

RESULT 9

AAU74417

ID AAU74417 standard; peptide; 117 AA.

XX AC AAU74417;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein heavy chain variable domain (VH) #2.

XX KW Antigen-binding protein; antibody heavy chain variable domain;

XX KW cytotstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

XX KW vascular endothelial growth factor receptor; VEGF;

XX KW cell proliferation inhibitor.

XX OS Mus sp.

XX PN WO200190192-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX WPI; 2002-106189/14.

DR N-PSDB; AAS20288.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX Claim 61; Page 60; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 51; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDYEGY 8
| | | | | | | |
Db 99 YGDYEGY 106

RESULT 10
AAE13145
ID AAE13145 standard; Protein; 136 AA.

XX AAE13145;

AC AAE13145;

DT 28-JAN-2002 (first entry)

XX Chimeric p1C11 heavy chain fragment.

Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
human; p1C11 vector.

XX Chimeric - Homo sapiens.
OS Chimeric - Unidentified.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Leader_peptide

FT Protein 20..136

FT Region /note= "Mature chimeric p1C11 heavy chain fragment"

FT Region 45..54

FT Region /label= CDR_H1

FT Region 69..85

FT Region /label= CDR_H2

FT Misc-difference 84

FT /note= "Residue 'O' is present at this location in the

FT sequence shown in fig-11 of the specification"

FT Misc-difference 101

FT /note= "Residue 'O' is present at this location in the

FT sequence shown in fig-11 of the specification"

FT Region 119..125

FT Region /label= CDR_H3

XX WO200174296-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.
PF
XX
XX 31-MAR-2000; 2000US-0540770.
PR
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.

DR N-PSDB; AAD21682.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
tumors such as leukemias or multiple myeloma comprises treatment with
an antagonist of a vascular endothelial growth factor receptor -

PS Example 3; Fig 11; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid
tumour cells that are stimulated by a ligand of vascular endothelial
growth factor receptor (VEGFR) in mammals particularly humans. The method
involves treating the mammals with humanised VEGFR monoclonal antibodies
(antagonists). Humanised monoclonal antibody comprises humanised mouse
variable region joined to human constant region, where the humanised
mouse variable region contains mouse complementarity determining region
(CDR) grafted into human variable region. The method is useful for
treating leukaemias such as acute or chronic myelocytic leukaemia, acute
or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
multiple myelomas and lymphoid cells, particularly those related to
non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
p1C11 heavy chain fragment which is used for the construction of chimeric
p1C11 IgG expression vector. Chimeric p1C11 heavy chain contains cloned
variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
domain (CH).

XX Sequence 136 AA;

Query Match 100.0%; Score 51; DB 22; Length 136;

Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDYEGY 8

| | | | | | | |
Db 118 YGDYEGY 125

RESULT 11

AAB82701

ID AAB82701 standard; Protein; 136 AA.

XX AAB82701;

XX 15-OCT-2001 (first entry)

VEGF antagonist antibody IMC-1C11 heavy chain variable region.

IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
vascular endothelial growth factor; angiogenesis; antiangiogenic;
antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
colon carcinoma; ovarian carcinoma; neuroblastoma;
glioblastoma multiforme; melanoma; therapy; heavy chain.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Signal_peptide

FT Protein 20..136

FT Region /label= Mature_protein

FT Region 45..54


```
FT      /label= CDR-H1
FT      /note= "complementarity determining region 1"
FT      Region
FT      59..85
FT      /label= CDR-H2
FT      /note= "complementarity determining region 2"
FT      Region
FT      118..125
FT      /label= CDR-H3
FT      /note= "complementarity determining region 3"
XX
PN      WO200154723-A1.
XX
XX      02-AUG-2001.
XX
XX      29-JAN-2001; 2001WO-US02839.
XX
XX      28-JAN-2000; 2000US-0178791.
PR      31-MAR-2000; 2000US-0539692.
XX
XX      (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA      (IMCL-) IMCLONE SYSTEMS INC.
XX
XX      Kerbel R;
PI
XX
DR      WPI; 2001-514531/56.
DR      N-PSDB; AAH26413.
XX
XX      Treating or controlling an angiogenic dependent condition (e.g. a
PT      neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT      administering a combination of an antiangiogenic molecule and a
PT      chemotherapeutic agent -
XX
PS      Disclosure; Fig 1; 42pp; English.
XX
XX      The present sequence is that of the heavy chain variable region of
CC      IMC-1C11, a mouse-human chimeric antibody that has vascular
CC      endothelial growth factor (VEGF) antagonist activity. The antibody,
CC      or a fragment of it, can be used as an anti-angiogenic molecule,
CC      together with a chemotherapeutic acid, for the treatment of an
CC      angiogenic dependent condition in a mammal, especially a human.
CC      The invention relates generally to a method of treating or
CC      controlling an angiogenic dependent condition by administering an
CC      anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC      regression or arrest of the condition while minimising or
CC      preventing significant toxicity of the chemotherapeutic agent.
CC      The anti-angiogenic molecule inhibits or blocks the action of a
CC      vascular endothelium survival factor such as VEGF or its receptor,
CC      and is especially IMC-1C11. Conditions that can be treated include
CC      a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC      especially a solid tumour, including breast carcinoma, lung
CC      carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC      ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC      neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ      Sequence 136 AA;

      Query Match      100.0%; Score 51; DB 22; Length 136;
      Best Local Similarity 100.0%; Pred. No. 0.63;
      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YYG DYEGY 8
      |||||
Db      118 YYG DYEGY 125

      RESULT 12
AAU74420
ID      AAU74420 standard; Protein; 238 AA.
XX
AC      AAU74420;
XX
XX      26-MAR-2002 (first entry)
XX
DE      Antigen-binding protein, single chain variable fragment version #2.
```

```
XX      Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW      cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW      vascular endothelial growth factor receptor; VEGF;
KW      cell proliferation inhibitor.
XX
OS      Mus sp.
OS      Synthetic.
XX
FH      Location/Qualifiers
FT      1..117
FT      /label= VH
FT      /note= "Heavy chain variable domain. Specifically
FT      claimed in claim 61"
FT      118..132
FT      /label= Linker
FT      /note= "15 amino acid linker joins the VH and VL
FT      regions of the single chain variable fragment
FT      protein. Encoded by AAS20285"
FT      133..238
FT      /label= VL
FT      /note= "Light chain variable domain. Specifically
FT      claimed in claim 61"
XX
PN      WO200190192-A2.
XX
XX      29-NOV-2001.
XX
XX      24-MAY-2001; 2001WO-US16924.
XX
XX      24-MAY-2000; 2000US-206749P.
XX      (IMCL-) IMCLONE SYSTEMS INC.
PA
XX      Zhu Z;
PI
XX      WPI; 2002-106189/14.
DR
XX      New bispecific immunoglobulin-like antigen-binding protein for reducing
PT      tumour growth and for inhibiting angiogenesis, comprises a complex of
PT      two polypeptides and two second polypeptides -
XX
PS      Claim 63; Page 62-63; 64pp; English.
XX
XX      The invention describes an antigen-binding protein (I) comprising a
CC      complex of two polypeptides (P1) and two second polypeptides (P2) which
CC      are stably associated in an immunoglobulin like complex. P1 has an
CC      antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC      light chain constant domain (CL domain), and P2 has an antigen-binding
CC      site located to the N terminus of the CH1 domain. (I) is useful for:
CC      neutralising the activation of a vascular endothelial growth factor
CC      (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC      reducing endothelial cell proliferation; inhibiting VEGF induced
CC      migration of human leukaemia cells; blocking interaction of a protein and
CC      its ligand; promoting interactions between immune cells and target cells;
CC      and in vivo and in vitro for investigative, diagnostic or treatment
CC      methods. The design of (I) provides for efficient production so that
CC      substantially all of the antigen-binding proteins produced are assembled
CC      in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC      and in tetrameric form. The heavy chain constant domains which constitute
CC      the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC      antibody and which provide other antibody functions can be present. There
CC      is no requirement for processing in vitro to obtain the complete product.
CC      This is the amino acid sequence of a single chain variable fragment
CC      (scFv), an engineered protein containing a variable light and variable
CC      heavy domain on one polypeptide, described in the method of the
CC      invention.
XX
SQ      Sequence 238 AA;

      Query Match      100.0%; Score 51; DB 23; Length 238;
      Best Local Similarity 100.0%; Pred. No. 1.1;
      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 YYGDYEGY 8
 |||||
Db 99 YYGDYEGY 106

RESULT 13
AAU74419
ID AAU74419 standard; Protein; 240 AA.
XX
AC AAU74419;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #1.
XX
KW Antigen-binding protein; single chain variable fragment; scFv; antigen;
KW cytotatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic
XX
FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"
FT 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 63; Page 62; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
CC invention.
XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 51; DB 23; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
 |||||
Db 99 YYGDYEGY 106

RESULT 14
AAR92576
ID AAR92576 standard; peptide; 11 AA.
XX
AC AAR92576;
XX
DT 10-SEP-1996 (first entry)
XX
DE VLA-4 binding peptide #39.
XX
KW VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR;
KW alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis;
KW complementarity determining region; inflammatory brain disorder; therapy;
KW multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis;
KW AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases;
KW rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "acetylated"
XX
PN WO9601644-A1.
XX
PD 25-JAN-1996.
XX
PF 10-JUL-1995; 95WO-US08516.
XX
PR 06-JUN-1995; 95US-0467580.
PR 11-JUL-1994; 94US-0273055.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Pleiss MA, Thorsett ED, Yednock TA;
XX
DR WPI; 1996-097452/10.
XX
PT New peptide(s) that bind VLA-4, inhibit leucocyte adhesion - useful
PT esp. for treatment of inflammatory disease, e.g. multiple sclerosis
XX
PS Claim 12; Page 28; 42pp; English.
XX
CC AAR92563-R92594 represents VLA-4 binding peptides derived from the FGN
CC region of VCAM-1. VLA-4 is also known as alpha4beta1 integrin and
CC CD49d/CD29. VLA-4 binds to the non-matrix molecule VCAM-1, which is
CC expressed by endothelial and other cells. These sequences mimic a short
CC consensus sequence in the FGN region of VCAM-1. These sequences inhibit
CC the adhesion of leucocytes mediated by VLA-4. It is useful for treating
CC inflammatory brain disorders (especially multiple sclerosis),
CC meningitis, encephalitis, asthma, Alzheimer's disease, atherosclerosis,
CC AIDS dementia, diabetes, inflammatory bowel disease, rheumatoid

CC arthritis, transplant rejection, tumour metastases and myocardial
CC ischaemia. These sequences can also be labelled, and can then be used
CC for in vivo or in vitro diagnosis, such as monitoring inflammatory
CC responses, isolating leucocytes, in assays for inhibitors of VLA-4/VCAM-1
CC interactions and imaging sites of inflammation.

XX Sequence 11 AA;

Query Match 76.5%; Score 39; DB 17; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||:| ||
Db 3 YYGNYGGY 10

RESULT 15
AAR13721
ID AAR13721 standard; Protein; 120 AA.
XX
AC AAR13721;
XX
DT 06-NOV-1991 (first entry)
XX
DE Control fusion protein putative binding site.
XX
KW Heterofunctional; totally synthetic affinity reagents; TSAR.
XX
OS Synthetic.
XX
PN WO9112328-A.
XX
PD 22-AUG-1991.
XX
PF 14-FEB-1991; 91WO-US01013.
XX
PR 15-FEB-1990; 90US-0480420.
XX
PA (FOWL/) FOWLKES D M.
XX
PI Fowlkes D, Kay BK;
XX
DR WPI; 1991-267139/36.
DR N-PSDB; AAQ13360.
XX

PT Prodn. of hetero-functional binding fusion proteins - used for in
PT vitro and in vivo applications, e.g. diagnosis and vaccine prodn.
XX

PS Disclosure; Fig 2; 81pp; English.

XX
CC This amino acid sequence codes for the N-terminal end of the
CC control fusion protein. It was obtd. from the DNA and makes up the
CC putative binding domain of the control fusion protein. The fusion
CC proteins, termed Totally Synthetic Affinity Reagents (TSARs) are
CC useful for in vitro and in vivo applications that make use of
CC binding regions of antibodies, DNA binding proteins, adhesive
CC proteins, etc. e.g. in the field of biomedicine, bioregulation and
CC control. Also in the prodn. of vaccines, (immunogens) in separations
CC and purifications, and in diagnostics. The method is quick, simple,
CC efficient and relatively inexpensive. A great diversity of binding
CC characteristics can be obtd. There is no need for detailed
CC knowledge of the function of portions of the binding sequence or
CC the amino acids that are involved in ligand binding in order to
CC produce the TSARs. See also AAR13722.

XX Sequence 120 AA;

Query Match 74.5%; Score 38; DB 12; Length 120;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8

Db 99 YYDYEGF 106
||| ||||:

Search completed: December 23, 2002, 07:25:04
Job time : 5.29457 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 1.44186 Seconds
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Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YYGDIYEGY 8

Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	39	76.5	11	3	US-08-467-580-43	Sequence 43, Appl
2	39	76.5	11	5	PCT-US95-08516-43	Sequence 43, Appl
3	36	70.6	525	4	US-09-113-750A-35	Sequence 35, Appl
4	36	70.6	663	4	US-09-134-078-61	Sequence 61, Appl
5	36	70.6	680	4	US-09-134-078-25	Sequence 25, Appl
6	36	70.6	933	2	US-08-313-200-1	Sequence 1, Appli
7	36	70.6	933	5	PCT-US93-03837-1	Sequence 1, Appli
8	35	68.6	1507	6	5268270-2	Patent No. 5268270
9	34	66.7	116	2	US-08-888-366-12	Sequence 12, Appl
10	34	66.7	139	4	US-09-136-315-2	Sequence 2, Appli
11	34	66.7	139	4	US-09-136-315-6	Sequence 6, Appli
12	34	66.7	660	4	US-09-134-001C-3350	Sequence 3350, Ap
13	33.5	65.7	261	2	US-07-857-224B-61	Sequence 61, Appl
14	33	64.7	11	3	US-08-467-580-42	Sequence 42, Appl
15	33	64.7	11	5	PCT-US95-08516-42	Sequence 42, Appl
16	33	64.7	371	1	US-08-225-477B-8	Sequence 8, Appli
17	33	64.7	371	5	PCT-US95-04353-8	Sequence 8, Appli
18	33	64.7	389	4	US-09-055-765-13	Sequence 13, Appl
19	33	64.7	400	4	US-09-264-097-6	Sequence 6, Appli
20	33	64.7	402	4	US-09-055-765-14	Sequence 14, Appl
21	33	64.7	405	4	US-09-291-023A-20	Sequence 20, Appl
22	33	64.7	485	2	US-08-446-803-1	Sequence 1, Appli
23	33	64.7	485	2	US-08-446-803-2	Sequence 2, Appli
24	33	64.7	485	2	US-08-861-837-1	Sequence 1, Appli
25	33	64.7	485	2	US-08-861-837-2	Sequence 2, Appli
26	33	64.7	485	2	US-08-600-908A-12	Sequence 12, Appl
27	33	64.7	485	3	US-08-683-838A-12	Sequence 12, Appl

28	33	64.7	485	3	US-08-600-656-1	Sequence 1, Appli
29	33	64.7	485	3	US-08-600-656-2	Sequence 2, Appli
30	33	64.7	485	3	US-08-600-656-7	Sequence 7, Appli
31	33	64.7	485	4	US-09-170-670-1	Sequence 1, Appli
32	33	64.7	485	4	US-09-170-670-2	Sequence 2, Appli
33	33	64.7	485	4	US-09-170-670-6	Sequence 6, Appli
34	33	64.7	485	4	US-09-170-670-7	Sequence 7, Appli
35	33	64.7	485	4	US-09-170-670-8	Sequence 8, Appli
36	33	64.7	485	4	US-09-193-068-1	Sequence 1, Appli
37	33	64.7	485	4	US-09-193-068-2	Sequence 2, Appli
38	33	64.7	485	4	US-09-193-068-6	Sequence 6, Appli
39	33	64.7	485	4	US-09-193-068-7	Sequence 7, Appli
40	33	64.7	485	4	US-09-193-068-8	Sequence 8, Appli
41	33	64.7	485	4	US-09-183-412-1	Sequence 1, Appli
42	33	64.7	485	4	US-09-183-412-2	Sequence 2, Appli
43	33	64.7	485	4	US-09-183-412-6	Sequence 6, Appli
44	33	64.7	485	4	US-09-183-412-7	Sequence 7, Appli
45	33	64.7	485	4	US-09-183-412-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-467-580-43
; Sequence 43, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: derived from VCAM-1
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLTATION
US-08-467-580-43

Query Match 76.5%; Score 39; DB 3; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||:|
Db 3 YYGNYGGY 10

RESULT 2
PCT-US95-08516-43
; Sequence 43, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATHENA NEUROSCIENCES, INC.
; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
; STREET: 800 Gateway Blvd.
; CITY: South San Francisco
; STATE: CA

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08516
; FILING DATE: 10-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/273,055
; FILING DATE: 11-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 002010-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-3620
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-08516-43

Query Match 76.5%; Score 39; DB 5; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
||| ||
Db 3 YGNYGGY 10

RESULT 3
US-09-113-750A-35
; Sequence 35, Application US/09113750A
; Patent No. 6294176
; GENERAL INFORMATION:
; APPLICANT: David E. Junker and Mark D. Cochran
; TITLE OF INVENTION: Recombinant Raccoonpox virus
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,750A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 55744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)262-0400
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-113-750A-35

Query Match 70.6%; Score 36; DB 4; Length 525;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| ||||| |
Db 71 YSGDIYENY 78

RESULT 4
US-09-134-078-61
; Sequence 61, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-134-078-61

Query Match 70.6%; Score 36; DB 4; Length 663;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
|| ||| |
Db 361 YPDIYDGF 368

RESULT 5
US-09-134-078-25
; Sequence 25, Application US/09134078
; Patent No. 6368844


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;
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-09-134-078-25
;
; Query Match 70.6%; Score 36; DB 4; Length 680;
; Best Local Similarity 62.5%; Pred. No. 2.7e+02;
; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 YYGDYEGY 8
Db 378 YYPDYDGF 385
;
RESULT 6
US-08-313-200-1
; Sequence 1, Application US/08313200
; Patent No. 5998153
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,200
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```
;
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20658.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 933 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Mature
; TISSUE TYPE: Thyroid gland(from people with Grave's
; TISSUE TYPE: disease)
; IMMEDIATE SOURCE:
; CLONE: pHTPO-2.8
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: join(1..3, 456..631)
; OTHER INFORMATION: /note= "TPO region within fusion
; plasmid: TPO(delta4-455)"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
; OTHER INFORMATION: /note= "C-terminal truncation:
; TPO(1-120)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..400
; OTHER INFORMATION: /note= "TPO epitopic region within
; fusion protein: MBP-TPO (AA 1-400)"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..455
; OTHER INFORMATION: /note= "C-terminal truncation-
; TPO(1-455) or N-terminal half of TPO"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..631
; OTHER INFORMATION: /note= "C-terminal truncation:
; TPO(1-631)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 266..281
; OTHER INFORMATION: /note= "TPO epitopic or binding
; region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 376..631
; OTHER INFORMATION: /note= "TPO epitopic region within
; fusion protein: MBP-TPO (AA 376-631)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: join(455..532, 590..933)
; OTHER INFORMATION: /note= "alternatively spliced
; C-terminus of TPO"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 455..933
; OTHER INFORMATION: /note= "TPO C-terminus containing
; binding region"
; FEATURE:
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; NAME/KEY: Region
; LOCATION: 456..631 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 456..633 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 456..933 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 456..933 /note= "TPO region within maltose
; OTHER INFORMATION: binding fusion protein"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 457..517 /note= "non-reactive fragment"
; OTHER INFORMATION:
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 457..633 /note= "TPO region within fusion
; OTHER INFORMATION: plasmid pMaltPO"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 457..933 /note= "TPO binding region within
; OTHER INFORMATION: plasmid pMaltPO"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 465..933 /note= "TPO binding region of
; OTHER INFORMATION: maltose binding region fusion construct"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 513..633 /note= "recombinant TPO"
; OTHER INFORMATION:
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 517..630 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 517..633 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 573..633 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 590..611 /note= "TPO region within maltose
; OTHER INFORMATION: binding fusion protein"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 590..615 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Binding-site
; LOCATION: 590..675 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:

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; NAME/KEY: Region
; LOCATION: 592..613 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 596..611 /note= "Tpo region within fusion
; OTHER INFORMATION: protein"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 602..615 /note= "TPO region containing
; OTHER INFORMATION: divergent sequences"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 611..615 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 631..933 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 632..933 /note= "TPO region within maltose
; OTHER INFORMATION: binding fusion protein"
; FEATURE:
;
; NAME/KEY: Region
; LOCATION: 633..768 /note= "TPO binding or epitopic
; OTHER INFORMATION:
;
Query Match 70.6%; Score 36; DB 2; Length 933;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
   | | | | |
Db 466 YVGPYEGY 473

RESULT 7
PCT-US93-03837-1
; Sequence 1, Application PC/TUS9303837
; GENERAL INFORMATION:
; APPLICANT: Baker, Jr., James R.
; APPLICANT: Koenig, Ronald J.
; TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03837
; FILING DATE: 19930422
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewak, Anna M.
; REGISTRATION NUMBER: 33006
; REFERENCE/DOCKET NUMBER: 2115-00658PPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 641-1600

```

TELEFAX: (313) 641-0270
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 933 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Mature
; TISSUE TYPE: Thyroid gland (from people with Grave's
; TISSUE TYPE: disease)
; IMMEDIATE SOURCE:
; CLONE: pHTPO-2.8
; PUBLICATION INFORMATION:
; AUTHORS: Kimura, S.
; AUTHORS: Kotani, T.
; AUTHORS: McBride, O. W.
; AUTHORS: Umeki, K.
; AUTHORS: Nakayama, T.
; AUTHORS: Ohtaki, S.
; AUTHORS: Hirai, K.
; TITLE: Human thyroid peroxidase: Complete cDNA and
; TITLE: protein sequence, chromosome mapping, and
; TITLE: identification of two alternately spliced mRNAs
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 84
; PAGES: 5555-5559
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 3048
PCT-US93-03837-1

Query Match 70.6%; Score 36; DB 5; Length 933;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
| | | | |
Db 466 YVGPIYEGY 473

RESULT 8
5268270-2
; Patent No. 5268270
; APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johannes
; TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
; NEGATIVE HOST CELLS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/171,872
; FILING DATE: 01-JUL-1987
; SEQ ID NO: 2:
; LENGTH: 1507
5268270-2

Query Match 68.6%; Score 35; DB 6; Length 1507;
Best Local Similarity 62.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
| | | | |
Db 110 YYGQYNGH 117

RESULT 9
US-08-888-366-12
; Sequence 12, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.

APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-12

Query Match 66.7%; Score 34; DB 2; Length 116;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
| | | | |
Db 96 YYGNYEWF 103

RESULT 10
US-09-136-315-2
; Sequence 2, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILLIANO
; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
; TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
; FILE REFERENCE: 0010-0933-0
; CURRENT APPLICATION NUMBER: US/09/136,315B
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-136-315-2

Query Match 66.7%; Score 34; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
||| |
Db 119 YGSGYGGF 126

RESULT 11

US-09-136-315-6
; Sequence 6, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILLIANO
; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
; TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
; FILE REFERENCE: 0010-0933-0
; CURRENT APPLICATION NUMBER: US/09/136,315B
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 6
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-136-315-6

Query Match 66.7%; Score 34; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
||| |
Db 119 YGSGYGGF 126

RESULT 12

US-09-134-001C-3350
; Sequence 3350, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3350
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3350

Query Match 66.7%; Score 34; DB 4; Length 660;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
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Db 123 YLGEYEGW 130

RESULT 13

US-07-857-224B-61
; Sequence 61, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Caenorhabditis elegans
; FEATURE: Protein kinase; Table 8 Column 69
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-61

Query Match 65.7%; Score 33.5; DB 2; Length 261;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 YGD-YEGY 8
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Db 14 YGDVYEGY 21

RESULT 14

US-08-467-580-42
; Sequence 42, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055

Search completed: December 23, 2002, 07:33:13
Job time : 2.44186 secs

EARLIER FILING DATE: 1994-07-11
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: derived from VCAM-1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
US-08-467-580-42

Query Match 64.7%; Score 33; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 3 YYGNYGAY 10

RESULT 15
PCT-US95-08516-42
Sequence 42, Application PC/TUS9508516
GENERAL INFORMATION:
APPLICANT: ATHENA NEUROSCIENCES, INC.
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES, INC.
STREET: 800 Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08516
FILING DATE: 10-JUL-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,055
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 002010-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-3620
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-08516-42

Query Match 64.7%; Score 33; DB 5; Length 11;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 3 YYGNYGAY 10

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 0.744186 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YGDIYEGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	51	100.0	8	10	US-09-976-787-3
2	51	100.0	8	10	US-09-865-198-3
3	51	100.0	117	10	US-09-976-787-7
4	51	100.0	117	10	US-09-976-787-23
5	51	100.0	117	10	US-09-865-198-7
6	51	100.0	117	10	US-09-865-198-22
7	51	100.0	238	10	US-09-976-787-29
8	51	100.0	238	10	US-09-865-198-28
9	51	100.0	240	10	US-09-976-787-28
10	51	100.0	240	10	US-09-865-198-27
11	37	72.5	335	10	US-09-821-687-11
12	37	72.5	633	10	US-09-821-687-10
13	36	70.6	663	9	US-10-121-032-61
14	36	70.6	680	9	US-10-121-032-25
15	35	68.6	214	10	US-09-925-299-990
16	34	66.7	652	10	US-09-815-242-5896
17	34	66.7	657	10	US-09-815-242-12135
18	34	66.7	657	10	US-09-815-242-13013
19	34	66.7	666	10	US-09-815-242-4933

20	34	66.7	677	10	US-09-815-242-10663	Sequence 10663, A
21	33	64.7	148	12	US-10-052-586-360	Sequence 360, App
22	33	64.7	197	9	US-09-918-543-13	Sequence 13, Appl
23	33	64.7	389	10	US-09-143-127-12	Sequence 12, Appl
24	33	64.7	389	12	US-10-036-507-13	Sequence 13, Appl
25	33	64.7	392	10	US-09-945-825-8	Sequence 8, Appl
26	33	64.7	402	10	US-09-143-127-10	Sequence 10, Appl
27	33	64.7	402	10	US-09-143-127-14	Sequence 14, Appl
28	33	64.7	402	12	US-10-036-507-14	Sequence 14, Appl
29	33	64.7	485	9	US-09-918-543-2	Sequence 2, Appl
30	33	64.7	485	9	US-09-918-543-4	Sequence 4, Appl
31	33	64.7	485	9	US-09-918-543-12	Sequence 12, Appl
32	33	64.7	485	9	US-09-795-211-1	Sequence 1, Appl
33	33	64.7	485	9	US-09-795-211-2	Sequence 2, Appl
34	33	64.7	485	10	US-09-769-864-1	Sequence 1, Appl
35	33	64.7	485	10	US-09-769-864-2	Sequence 2, Appl
36	33	64.7	485	10	US-09-769-864-6	Sequence 6, Appl
37	33	64.7	485	10	US-09-769-864-7	Sequence 7, Appl
38	33	64.7	485	10	US-09-769-864-8	Sequence 8, Appl
39	33	64.7	485	10	US-09-854-346-2	Sequence 2, Appl
40	33	64.7	485	10	US-09-854-346-4	Sequence 4, Appl
41	33	64.7	485	10	US-09-854-346-12	Sequence 12, Appl
42	33	64.7	485	10	US-09-854-346-13	Sequence 13, Appl
43	33	64.7	485	10	US-09-902-188A-1	Sequence 1, Appl
44	33	64.7	485	10	US-09-902-188A-2	Sequence 2, Appl
45	33	64.7	485	10	US-09-902-188A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-3
; Sequence 3, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-3

Query Match	100.0%;	Score 51;	DB 10;	Length 8;
Best Local Similarity	100.0%;	Pred. NO. 8.9e+04;		
Matches	8;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	YGDYEGY 8		
Db	1	YGDYEGY 8		

RESULT 2
US-09-865-198-3
; Sequence 3, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-3

Query Match 100.0%; Score 51; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. NO. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 1 YYGDYEGY 8

RESULT 3
US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 99 YYGDYEGY 106

RESULT 4
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse

US-09-976-787-23

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 99 YYGDYEGY 106

RESULT 5
US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 99 YYGDYEGY 106

RESULT 6
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 99 YYGDYEGY 106

RESULT 7
US-09-976-787-29

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; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match          100.0%; Score 51; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGDYEGY 8
        |||||
Db       99 YGDYEGY 106

RESULT 8
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match          100.0%; Score 51; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGDYEGY 8
        |||||
Db       99 YGDYEGY 106

RESULT 9
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
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; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match          100.0%; Score 51; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGDYEGY 8
        |||||
Db       99 YGDYEGY 106

RESULT 10
US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match          100.0%; Score 51; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGDYEGY 8
        |||||
Db       99 YGDYEGY 106

RESULT 11
US-09-821-687-11
; Sequence 11, Application US/09821687
; Patent No. US20020106724A1
; GENERAL INFORMATION:
; APPLICANT: MIKOSHIBA, KATSUHIKO
; APPLICANT: MIZUTANI, AKIHIRO
; TITLE OF INVENTION: RNA-BINDING PROTEIN
; FILE REFERENCE: 081356/0162
; CURRENT APPLICATION NUMBER: US/09/821,687
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-299812
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: m-hnRNPR
US-09-821-687-11

Query Match          72.5%; Score 37; DB 10; Length 335;
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Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|| || ||
Db 172 YYDDYGY 179

RESULT 12
US-09-821-687-10
; Sequence 10, Application US/09821687
; Patent No. US20020106724A1
; GENERAL INFORMATION:
; APPLICANT: MIKOSHIBA, KATSUHIKO
; APPLICANT: MIZUTANI, AKIHIRO
; TITLE OF INVENTION: RNA-BINDING PROTEIN
; FILE REFERENCE: 081356/0162
; CURRENT APPLICATION NUMBER: US/09/821,687
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-299812
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: hnrNPR
US-09-821-687-10

Query Match 72.5%; Score 37; DB 10; Length 633;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|| || ||
Db 470 YYDDYGY 477

RESULT 13
US-10-121-032-61
; Sequence 61, Application US/10121032
; Patent No. US20020155550A1
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/121,032
; FILING DATE: 09-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-121-032-61

Query Match 70.6%; Score 36; DB 9; Length 663;
Best Local Similarity 62.5%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|| || ||
Db 361 YYPDYDGF 368

RESULT 14
US-10-121-032-25
; Sequence 25, Application US/10121032
; Patent No. US20020155550A1
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/121,032
; FILING DATE: 09-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-121-032-25

Query Match 70.6%; Score 36; DB 9; Length 680;

Best Local Similarity 62.5%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YYGDYEGY 8
|| |||:
Db 378 YYPDYDGF 385

RESULT 15
US-09-925-299-990
; Sequence 990. Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 990
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-990

Query Match 68.6%; Score 35; DB 10; Length 214;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YYGDYEGY 8
||| | |:
Db 105 YGYHGF 112

Search completed: December 23, 2002, 07:58:18
Job time : 0.744186 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 1.5814 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-3

Perfect score: 51

Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	80.4	435	2	D81272	hypothetical prote
2	40	78.4	542	2	S63222	MPA43 protein - ye
3	40	78.4	616	1	SYTWT	methionine-tRNA li
4	40	78.4	1650	2	T18444	hypothetical prote
5	39	76.5	63	2	S44634	f22b7.4 protein -
6	38	74.5	595	2	B70402	hypothetical prote
7	38	74.5	660	2	E83656	methionyl-tRNA syn
8	38	74.5	3216	2	C90538	hypothetical prote
9	37	72.5	89	2	T19805	hypothetical prote
10	37	72.5	110	2	S13688	Ig heavy chain V r
11	37	72.5	154	1	A69012	conserved hypothet
12	37	72.5	271	2	S38115	hypothetical prote
13	37	72.5	542	2	B81910	probable ABC-trans
14	37	72.5	542	2	E81105	ABC transporter, A
15	37	72.5	564	2	T26053	hypothetical prote
16	37	72.5	633	2	T02673	heterogeneous nucl
17	37	72.5	730	2	A48832	cell surface glyco
18	37	72.5	1657	2	T19536	hypothetical prote
19	36	70.6	15	2	PH1366	Ig heavy chain DJ
20	36	70.6	120	2	A54256	Ig heavy chain V r
21	36	70.6	191	2	AE1218	alpha-ribazole-5'-
22	36	70.6	191	2	AH1571	alpha-ribazole-5'-
23	36	70.6	252	2	A95071	amino acid ABC tra
24	36	70.6	441	2	T49265	hypothetical prote
25	36	70.6	565	2	G90518	5'-nucleotidase pr
26	36	70.6	587	2	F69631	gamma-glutamyltran
27	36	70.6	656	2	T03473	acetate-CoA ligase
28	36	70.6	669	2	D72278	endo-1,4-beta-mann
29	36	70.6	831	2	AB3513	ATPase virB4 homol

30	36	70.6	851	2	T51545	receptor protein k
31	36	70.6	868	2	A84518	probable receptor-
32	36	70.6	914	1	JN0550	iodide peroxidase
33	36	70.6	914	1	S07047	iodide peroxidase
34	36	70.6	933	1	OPHUIT	iodide peroxidase
35	35	68.6	113	2	G82387	hypothetical prote
36	35	68.6	126	2	S16280	Ig heavy chain (38
37	35	68.6	145	2	S03844	Ig heavy chain pre
38	35	68.6	186	2	AB1210	dTDP-sugar epimera
39	35	68.6	188	2	H91066	hypothetical prote
40	35	68.6	201	2	H85910	unknown protein en
41	35	68.6	376	2	S69529	hypothetical prote
42	35	68.6	386	2	T14243	ubiquinol-cytochro
43	35	68.6	398	2	A75128	probable transamin
44	35	68.6	401	2	D71003	probable transamin
45	35	68.6	402	1	I61573	homeotic protein 1

ALIGNMENTS

RESULT 1

D81272

hypothetical protein Cj1295 [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C;Accession: D81272

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: D81272

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-435 <PAR>

A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73722.1; PID:g696

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj1295

C;Superfamily: Campylobacter jejuni hypothetical protein Cj1295

Query Match 80.4%; Score 41; DB 2; Length 435;

Best Local Similarity 85.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGDYEGY 8

||||:|

Db 325 YGDYDGY 331

RESULT 2

S63222

MPA43 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein N0875; protein YNL249c

C;Species: Saccharomyces cerevisiae

C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 06-Feb-1998

C;Accession: S63222; S61594

R;Sen-Gupta, M.; Gueldener, U.; Beinhauer, J.; Fiedler, T.; Hegemann, J.H.

submitted to the Protein Sequence Database, April 1996

A;Reference number: S63220

A;Accession: S63222

A;Molecule type: DNA

A;Residues: 1-542 <SEN>

A;Cross-references: EMBL:Z71525; NID:gl302290; PID:e239640; PID:gl302291; MIPS:YNL249

A;Experimental source: strain S288C

R;Boles, E.; Hettmann, C.; Zimmermann, F.K.

submitted to the EMBL Data Library, December 1995

A;Reference number: S61594

A;Accession: S61594

A;Molecule type: DNA

A;Residues: 'YQD',45,'SR',48,'HG NLA',54-542 <BOL>

A;Cross-references: EMBL:X94214; NID:gl122898; PID:e214032; PID:gl122899

C;Genetics:
A;Gene: SGD:MPA43
A;Cross-references: SGD:S0005193; MIPS:YNL249c
A;Map position: 14L

Query Match 78.4%; Score 40; DB 2; Length 542;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEG 7
:|||||
Db 360 FYG DYEG 366

RESULT 3

SYTWT
methionine-tRNA ligase (EC 6.1.1.10) - Thermus aquaticus
N;Alternate names: methionyl-tRNA synthetase
C;Species: Thermus aquaticus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
C;Accession: A39517
R;Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T.
J. Biol. Chem. 266, 3268-3277, 1991
A;Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilus.
A;Reference number: A39517; MUID:91131636; PMID:1993699
A;Accession: A39517
A;Molecule type: DNA
A;Residues: 1-616 <NUR>
A;Cross-references: GB:M64273; GB:J05744; NID:gl155135; PIDN:AAA27510.1; PID:gl155136
A;Experimental source: strain HB8, ATCC 27634
A;Note: the authors translated the codon TAC for residue 323 as Thr
C;Genetics:
A;Gene: mets
C;Superfamily: methionine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F;13,19,50,300/Active site: Tyr, His, Asp, Lys #status predicted

Query Match 78.4%; Score 40; DB 1; Length 616;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEG 7
:|||||
Db 118 YG DYEG 124

RESULT 4

T18444
hypothetical protein C0385c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18444
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18444
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1650 <LAW>
A;Cross-references: EMBL:Z98547; NID:e1325376; PID:e1427940; PIDN:CAB11112.2
C;Genetics:
A;Map position: 3
A;Introns: 1597/3; 1625/3
A;Note: C0385c

Query Match 78.4%; Score 40; DB 2; Length 1650;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YG DYEG 8
:|||||
Db 525 YG DYEG 532

RESULT 5

S44634
f22b7.4 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C;Accession: S44634
R;Anderson, K.
submitted to the EMBL Data Library, March 1993
A;Description: Sequence of the C. elegans cosmid F22B7.
A;Reference number: S44628
A;Accession: S44634
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <AND>
A;Cross-references: EMBL:L12018; NID:gl156298; PID:gl156305
C;Genetics:
A;Introns: 21/2

Query Match 76.5%; Score 39; DB 2; Length 63;
Best Local Similarity 75.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YG DYEG 8
:|||||
Db 56 YG DYEG 63

RESULT 6

B70402
hypothetical protein aq_1185 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000
C;Accession: B70402
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70402
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-595 <AQF>
A;Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07204.1; PID:g2983636; GB:AE00
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1185
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1185

Query Match 74.5%; Score 38; DB 2; Length 595;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YG DYEG 8
:|||||
Db 159 YG DYEG 165

RESULT 7

E83656
methionyl-tRNA synthetase mets [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E83656
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83656
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-660 <STO>

A;Cross-references: GB:AP001507; GB:BA0000004; NID:g10172612; PIDN:BAB03772.1; GSPDB:GN001507
A;Experimental source: strain C-125
C;Genetics:
A;Gene: mets
C;Superfamily: methionine-tRNA ligase

Query Match 74.5%; Score 38; DB 2; Length 660;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
| | | | |
Db 121 YLGDYEGW 128

RESULT 8
C90538
hypothetical protein MYPV_2110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: C90538
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: C90538
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3216 <KUR>
A;Cross-references: GB:AL445566; PID:g14089624; PIDN:CAC13384.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV_2110
A;Genetic code: SGC3

Query Match 74.5%; Score 38; DB 2; Length 3216;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
| | | | |
Db 1978 YYVDYEGF 1985

RESULT 9
T19805
hypothetical protein C37A5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19805
R;White, S.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19180
A;Accession: T19805
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-89 <WIL>
A;Cross-references: EMBL:Z92828; PIDN:CAB07335.1; GSPDB:GN00019; CESP:C37A5.8
A;Experimental source: clone C37A5
C;Genetics:
A;Gene: CESP:C37A5.8
A;Map position: 1
A;Introns: 52/2

Query Match 72.5%; Score 37; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
| | | | |
Db 61 YYGGYGGY 68

RESULT 10
S13688
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S13688
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13688
A;Molecule type: mRNA
A;Residues: 1-110 <PEN>
A;Cross-references: EMBL:X53341
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 110;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 YY-GDYEGY 8
| | | | |
Db 89 YYCXGDYDGY 98

RESULT 11
A69012
conserved hypothetical protein MTH1091 - Methanobacterium thermoautotrophicum (strain C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A69012
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.; J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69012
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-154 <MTH>
A;Cross-references: GB:AE000879; GB:AE000666; NID:g2622175; PIDN:AAB85580.1; PID:g2622
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1091
A;Start codon: GTG
C;Superfamily: conserved hypothetical protein MJ0375

Query Match 72.5%; Score 37; DB 1; Length 154;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEG 7
: | | | | :
Db 81 FYGDYDG 87

RESULT 12
S38115
hypothetical protein YKR043c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S38115
R;Urrestarazu, L.A.; Jauniaux, J.C.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S38097
A;Accession: S38115
A;Molecule type: DNA
A;Residues: 1-271 <URR>
A;Cross-references: EMBL:Z28268; NID:g486490; PID:g486491; GSPDB:GN00011; MIPS:YKR043
A;Experimental source: strain S288C

C:Genetics:
A:Gene: MIPS:YKR043C
A:Cross-references: SGD:S0001751
A:Map position: 11R
C:Superfamily: phosphoglycerate mutase; phosphoglycerate mutase homology

Query Match 72.5%; Score 37; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGDYEG 7
| | | | |
Db 102 YGDYEG 107

RESULT 13
B81910
Probable ABC-transporter ATP-binding protein NMA1409 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: B81910
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: B81910
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-542 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84649.1; PID:g738006
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1409
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 542;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
| | | | |
Db 528 YLGDYESY 535

RESULT 14
E81105
ABC transporter, ATP-binding protein NMB1240 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81105
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: E81105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-542 <TET>
A:Cross-references: GB:AE002472; GB:AE002098; NID:g7226475; PIDN:AAF41621.1; PID:g722648
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1240
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 542;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
| | | | |

Db 528 YLGDYESY 535
| | | | |
RESULT 15
T26053
hypothetical protein W01C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26053
R:Sims, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20143
A:Accession: T26053
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-564 <WIL>
A:Cross-references: EMBL:Z49969; PIDN:CAA90270.1; GSPDB:GN00020; CESP:W01C9.2
A:Experimental source: clone W01C9
C:Genetics:
A:Gene: CESP:W01C9.2
A:Map position: 2
A:Introns: 30/1; 64/1; 100/3; 124/3; 229/3; 272/3; 536/2

Query Match 72.5%; Score 37; DB 2; Length 564;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGDYEGY 8
| | | | |
Db 67 YGDYEDY 73

Search completed: December 23, 2002, 07:31:35
Job time : 5.5814 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 0.790698 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	80.4	402	1 LHX5_HUMAN	Q9h2c1 homo sapien
2	41	80.4	402	1 LHX5_XENLA	P37137 xenopus lae
3	40	78.4	542	1 MP43_YEAST	P53583 saccharomyc
4	40	78.4	616	1 SYM_THETH	P23395 thermus the
5	39	76.5	63	1 YLW4_CAEEL	P34407 caenorhabdi
6	39	76.5	489	1 OCLN_POTTR	Q28793 potorous tr
7	37	72.5	271	1 YK23_YEAST	P36136 saccharomyc
8	37	72.5	394	1 ASSY_METAC	Q8tny5 methanosarc
9	37	72.5	399	1 LHX5_BRARE	P52889 brachydanio
10	37	72.5	446	1 SOX8_HUMAN	P57073 homo sapien
11	37	72.5	633	1 ROR_HUMAN	O43390 homo sapien
12	37	72.5	730	1 G13A_DICDI	P34115 dictyosteli
13	36	70.6	587	1 GGT_BACSU	P54422 bacillus su
14	36	70.6	656	1 ACSA_RHOCA	O68040 rhodobacter
15	36	70.6	914	1 PERT_MOUSE	P35419 mus musculu
16	36	70.6	914	1 PERT_RAT	P14650 rattus norv
17	36	70.6	933	1 PERT_HUMAN	P07202 homo sapien
18	35	68.6	321	1 K6PF_PASMU	Q9cph2 pasteurella
19	35	68.6	376	1 YO23_BPHP1	P51725 bacterioph
20	35	68.6	402	1 LHX5_MOUSE	P50459 mus musculu
21	35	68.6	405	1 LHX1_BRARE	Q90476 brachydanio
22	35	68.6	428	1 RF4_KLULA	P09806 kluyveromyc
23	35	68.6	464	1 XKDK_BACSU	P54331 bacillus su
24	35	68.6	685	1 ERF2_YEAST	P05453 saccharomyc
25	35	68.6	919	1 AMY_STRLI	Q05884 streptomyce
26	35	68.6	1532	1 IGA_NEIGO	P09790 neisseria g
27	35	68.6	2358	1 MOKD_SCHPO	Q9Y719 saccharomyc
28	34	66.7	314	1 YG20_YEAST	P53257 saccharomyc
29	34	66.7	335	1 HTPX_ARCFU	O30004 archaeoglob
30	34	66.7	497	1 SYM_AQUAE	O67298 aquifex aeo
31	34	66.7	649	1 SYM_BACST	P23920 bacillus st
32	34	66.7	784	1 SX15_DROME	P40657 drosophila
33	34	66.7	972	1 UVRA_MYCTU	P94972 mycobacteri

34	34	66.7	3511	1 MY15_MOUSE	Q9qzz4 mus musculu
35	33.5	65.7	101	1 GP33_BPSP1	P06226 bacterioph
36	33.5	65.7	1196	1 ABL1_CAEEL	P03949 caenorhabdi
37	33	64.7	211	1 PMGY_SCHPO	P36623 schizosacch
38	33	64.7	216	1 RPOE_MYCTU	O05843 mycobacteri
39	33	64.7	265	1 LICD_HAEIN	P14184 haemophilus
40	33	64.7	350	1 EGSA_SULTO	P58460 sulfolobus
41	33	64.7	351	1 EGSA_SULSO	Q9uxe7 sulfolobus
42	33	64.7	367	1 HIS8_PARDE	Q51687 paracoccus
43	33	64.7	370	1 MYOM_APLCA	P15513 a myomoduli
44	33	64.7	379	1 SAT_PYRAB	P56863 pyrococcus
45	33	64.7	384	1 GLF1_KLEPN	Q48485 klebsiella

ALIGNMENTS

RESULT 1
LHX5_HUMAN
ID LHX5_HUMAN STANDARD; PRT; 402 AA.
AC Q9H2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5.
GN LHX5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11137295;
RA Zhao Y., Hermesz E., Yarolin M.C., Westphal H.;
RT "Genomic structure, chromosomal localization and expression of the
human LIM-homeobox gene LHX5.";
RL Gene 260:95-101(2000).
CC -!- FUNCTION: Plays an essential role in the regulation of neuronal
CC differentiation and migration during development of the central
CC nervous system.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in fetal brain and in various
CC regions of the adult central nervous system including the spinal
CC cord, the thalamus, and the cerebellum.
CC -!- SIMILARITY: CONTAINS 1 HOMEODOMAIN.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.

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CC EMBL; AF291181; AAG36963.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04180; -.
DR Genew; HGNC:14216; LHX5.
DR MIM; 605992; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEODOM_1; 1.
DR PROSITE; PS50071; HOMEODOM_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
DR

KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 402 AA; 44405 MW; E880138A1A3FCA2A CRC64;

Query Match 80.4%; Score 41; DB 1; Length 402;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEG 7
Db 278 YGDIYQG 284

RESULT 2
LHX5_XENLA STANDARD; PRT; 402 AA.

AC P37137;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5) (XLM-5) (XLM-2A).
GN LHX5 OR LIM5 OR LIM2A OR LIM-2A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95377545; PubMed=7649385;
RA Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.;
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in
RT Xenopus and zebrafish."
RL Dev. Biol. 170:583-593(1995).
RN [2]

RP SEQUENCE OF 188-225 FROM N.A.
RX MEDLINE=92192449; PubMed=1347750;
RA Taira M., Jamrich M., Good P.J., Dawid I.B.;
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed
RT specifically in the organizer region of Xenopus gastrula embryos."
RL Genes Dev. 6:356-366(1992).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS
CC SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
CC DIENCEPHALON.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.

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CC -----

DR EMBL; L42546; AAA99464.1; -.
DR EMBL; Z11587; CAA77672.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04209; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.

DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 402 AA; 44959 MW; A5852B94747E09F9 CRC64;

Query Match 80.4%; Score 41; DB 1; Length 402;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEG 7
Db 278 YGDIYQG 284

RESULT 3
MP43_YEAST STANDARD; PRT; 542 AA.

AC P53583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MPA43 protein.
GN MPA43 OR YNL249C OR N0875.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97377992; PubMed=9234673;
RA Sen-Gupta M., Guldener U., Beinhauer J.D., Fiedler T.A.,
RA Hegemann J.H.;
RT "Sequence analysis of the 33 kb long region between ORC5 and SUI1
RT from the left arm of chromosome XIV from Saccharomyces cerevisiae."
RL Yeast 13:849-860(1997).
RN [2]

RP SEQUENCE OF 41-542 FROM N.A.
RC STRAIN=ENY.WA-1A;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL; X96722; CAA65495.1; -.
DR EMBL; Z71525; CAA96156.1; -.
DR EMBL; X94214; CAA63905.1; -.
DR SGD; S0005193; MPA43.
FT CONFLICT 46 53 KSKWKFQW -> RSHGNLA (IN REF. 2).
SQ SEQUENCE 542 AA; 61667 MW; 830AA8D4E95365AD CRC64;

Query Match 78.4%; Score 40; DB 1; Length 542;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEG 7
Db 360 YGDIYEG 366

RESULT 4
SYM_THETH

```
ID AC P23395; STANDARD; PRT; 616 AA.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (METS).
GN METG OR METS.
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HB8 / ATCC 27634;
RX MEDLINE=91131636; PubMed=1993699;
RA Nureki O., Muramatsu T., Suzuki K., Kohda D., Matsuzawa H.,
RA Ohta T., Miyazawa T., Yokoyama S.;
RT "Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus
RT thermophilus HB8. Molecular cloning, primary-structure analysis,
RT expression in Escherichia coli, and site-directed mutagenesis.";
RL J. Biol. Chem. 266:3268-3277(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN-HB8 / ATCC 27634;
RX MEDLINE=20139706; PubMed=10673435;
RA Suglira I., Nureki O., Ugaji-Yoshikawa Y., Kuwabara S., Shimada A.,
RA Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;
RT "The 2.0-A crystal structure of Thermus thermophilus methionyl-tRNA
RT synthetase reveals two RNA-binding modules.";
RL Structure 8:197-208(2000).
CC -!- FUNCTION: IT IS PROBABLY ESSENTIAL FOR CELL SURVIVAL, BEING
CC REQUIRED NOT ONLY FOR ELONGATION OF PROTEIN SYNTHESIS BUT ALSO
CC FOR THE INITIATION OF ALL MRNA TRANSLATION THROUGH INITIATOR
CC TRNA(FMET) AMINOACYLATION.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE.
CC STRONG, TO CYSTEINYL-TRNA SYNTHETASE.
-----
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-----
DR EMBL; M64273; AAA27510.1; -
DR PIR; A39517; SYTWTM.
DR PDB; 1A8H; 04-MAY-99.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PRINTS; PR01041; TRNASYNTHMET.
DR TIGRFAMS; TIGR00398; metG; 1.
DR TIGRFAMS; TIGR00399; metG_C-term; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW tRNA-binding; 3D-structure.
FT SITE 10 22 "HIGH" REGION.
FT SITE 297 301 "KMSKS" REGION.
FT BINDING 300 300 ATP (BY SIMILARITY).
FT DOMAIN 524 616 tRNA BINDING.
SQ SEQUENCE 616 AA; 70638 MW; 053982C62558B72A CRC64;
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Query Match 78.4%; Score 40; DB 1; Length 616;

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Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDYEG 7
   |||:|
Db 118 YGEYEG 124

RESULT 5
YLW4_CAEEL STANDARD; PRT; 63 AA.
AC P34407;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F22B7.4 in chromosome III.
GN F22B7.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
-----
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-----
DR EMBL; L12018; AAA65461.1; -
DR WormPep; F22B7.4; CE00157.
KW Hypothetical protein.
SQ SEQUENCE 63 AA; 6803 MW; 2F7579C4907024B0 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 63;
Best Local Similarity 75.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
   ||| | |
Db 56 YGGYNGY 63

RESULT 6
OCLN_POTTR STANDARD; PRT; 489 AA.
ID OCLN_POTTR STANDARD; PRT; 489 AA.
AC Q28793;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Occludin.
GN OCLN.
OS Potorous tridactylus (Potoroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous.
OX NCBI_TaxID=9310;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=960181088; PubMed=8601611;
RA Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,
RA Itoh M., Ikenmura S., Furuse M., Tsukita S.;
RT "Interspecies diversity of the occludin sequence: cDNA cloning of
RT human, mouse, dog, and rat-kangaroo homologues.";
RL J. Cell Biol. 133:43-47(1996).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE FORMATION AND REGULATION OF THE
CC TIGHT JUNCTION (TJ) PARACELLULAR PERMEABILITY BARRIER. INTERACTS
CC WITH ZO-1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
CC EPITHELIAL AND ENDOTHELIAL CELLS.
CC -!- DOMAIN: THE C-TERMINAL IS CYTOPLASMIC AND IS IMPORTANT FOR
CC INTERACTION WITH ZO-1. NECESSARY FOR THE TIGHT JUNCTION
CC LOCALIZATION. INVOLVED IN THE REGULATION OF THE PERMEABILITY
CC BARRIER FUNCTION OF THE TIGHT JUNCTION (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ELL / OCCLUDIN FAMILY.
CC
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CC
DR EMBL; U49183; AAC48565.1; -.
DR InterPro; IPR002958; Occludin.
DR Pfam; PF02168; Occludin; 1.
DR PRINTS; PR01258; OCCLUDIN.
KW Tight junction; Transmembrane; Coiled coil; Phosphorylation.
FT DOMAIN 1 51
FT TRANSMEM 52 74
FT DOMAIN 75 112
FT TRANSMEM 113 137
FT DOMAIN 138 147
FT TRANSMEM 148 172
FT DOMAIN 173 222
FT TRANSMEM 223 244
FT DOMAIN 245 489
FT DOMAIN 76 107
FT DOMAIN 407 434
SQ SEQUENCE 489 AA; 54075 MW; 4F0CA45A41094860 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 489;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
Db 96 YGGYNGY 103

RESULT 7
YK23_YEAST
ID YK23_YEAST STANDARD; PRT; 271 AA.
AC P36136;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hypothetical 31.0 kDa protein in GAP1-NAP1 intergenic region.
GN YKR043C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]

RP SEQUENCE FROM N.A.
RA Urrestarazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC
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CC
DR EMBL; Z28268; CAA82119.1; -.
DR PIR; S38115; S38115.
DR SGD; S0001751; YKR043C.
DR InterPro; IPR001345; PG/BPGM_mutase.
DR Pfam; PF00300; PGAM; 1.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 31022 MW; FF934DE2F5145C40 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGDYEG 7
Db 102 YGDYEG 107

RESULT 8
ASSY_METAC
ID ASSY_METAC STANDARD; PRT; 394 AA.
AC Q8TNY5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
DE ligase).
DE ARGG OR MA2142.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate -> AMP +
CC diphosphate + L-argininosuccinate.
CC -!- PATHWAY: Arginine biosynthesis; penultimate step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
CC
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CC -----
DR EMBL; AE010900; AAM05540.1; -.
DR PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
DR PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
KW Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SQ SEQUENCE 394 AA; 43994 MW; 2B995B9C138E7EF1 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDYEGY 8
   |||||
Db 81 GDYEGY 86

RESULT 9
LHX5_BRARE
ID LHX5_BRARE STANDARD; PRT; 399 AA.
AC P52889;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5).
GN LHX5 OR LIM5.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95377545; PubMed=7649385;
RA Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.;
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in
RT Xenopus and zebrafish.";
RL Dev. Biol. 170:583-593(1995).
CC -!- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS
CC SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
CC DIENCEPHALON.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC -----
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CC -----
DR EMBL; L42547; AAA99465.1; -.
DR HSSP; P06601; 1FJL.
DR ZFIN; ZDB-GENE-980526-484; lim5.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
```

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FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 399 AA; 44513 MW; C0D7BB1B86D032DA CRC64;

Query Match 72.5%; Score 37; DB 1; Length 399;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDYEG 7
   |||:|:|
Db 278 YGEYQG 284

RESULT 10
SOX8_HUMAN
ID SOX8_HUMAN STANDARD; PRT; 446 AA.
AC P57073; Q9NZW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor SOX-8.
GN SOX8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheng Y.-C., Badge R.M., Armour J.A.L., Scotting P.J.;
RT "SOX8: a newly identified human gene expressed in paediatric brain
RT tumours and a candidate for the mental retardation phenotype in
RT ATR-16.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Ellington A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 119-446 FROM N.A.
RX MEDLINE=20130119; PubMed=10662550;
RA Pfeifer D., Poulat F., Holinski-Feder E., Kooy F., Scherer G.;
RT "The SOX8 gene is located within 700 kb of the tip of chromosome 16p
RT and is deleted in a patient with ATR-16 syndrome.";
RL Genomics 63:108-116(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN CENTRAL NERVOUS SYSTEM, LIMB AND
CC FACIAL DEVELOPMENT. MAY BE INVOLVED IN MALE SEX DETERMINATION.
CC BINDS THE CONSENSUS MOTIF 5'-[AT][ATCAA][AT]G-3' (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: CONTAINS 1 HMG BOX.
CC -----
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CC -----
DR EMBL; AF226675; AAF35886.1; -.
DR EMBL; AE006465; AAK61260.1; -.
DR EMBL; Z99757; CAB75612.1; ALT_INIT.
DR EMBL; AF164104; AAF37424.1; -.
DR HSSP; P48436; 1SX9.
DR TRANSFAC; T04917; -.
DR Genew; HGNC:11203; SOX8.
```

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DR MIM; 605923;
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 102 170 HMG_BOX.
SQ SEQUENCE 446 AA; 47314 MW; AE453359051A6DB3 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 446;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
   ||| |||
Db 391 YGAYPGY 398

RESULT 11
ROR_HUMAN
ID ROR_HUMAN STANDARD; PRT; 633 AA.
AC O43390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein R (hnRNP R).
GN HNRPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98083170; PubMed=9421497;
RA Hassfeldt W., Chan E.K.L., Mathison D.A., Portman D., Dreyfuss G.,
RA Steiner G., Tan E.M.;
RT "Molecular definition of heterogeneous nuclear ribonucleoprotein R
(hnRNP R) using autoimmune antibody: immunological relationship with
hnRNP P";
RL Nucleic Acids Res. 26:439-445(1998).
CC -!- FUNCTION: COMPONENT OF RIBONUCLEOSOMES, WHICH ARE COMPLEXES OF AT
CC LEAST 20 OTHER DIFFERENT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS
CC (HNRNP). HNRNP PLAY AN IMPORTANT ROLE IN PROCESSING OF PRECURSOR
CC MRNA IN THE NUCLEUS.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
CC -!- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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EMBL; AF000364; AAC39540.1; -
HSSP; P09651; 1HA1.
Genew; HGNC:5047; HNRPR.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 3.
SMART; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.
FT DOMAIN 1 153 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 412 418 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 165 244 RNA-BINDING (RRM) 1.
FT DOMAIN 246 328 RNA-BINDING (RRM) 2.
FT DOMAIN 341 411 RNA-BINDING (RRM) 3.
FT DOMAIN 447 567 RNA-BINDING (RGG-BOX).
FT DOMAIN 462 497 3 X 11 AA APPROXIMATE REPEATS OF D-D-Y-Y-
G-Y-D-Y-H-D-Y.
FT REPEAT 462 471 1 (APPROXIMATE).
FT REPEAT 472 482 2.
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FT REPEAT 488 497 3 (APPROXIMATE).
FT DOMAIN 579 633 GLN/ASN-RICH DOMAIN.
SQ SEQUENCE 633 AA; 70943 MW; 088341F6465ED46F CRC64;

Query Match 72.5%; Score 37; DB 1; Length 633;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
   ||| |||
Db 470 YDDYGY 477

RESULT 12
G13A_DICDI
ID G13A_DICDI STANDARD; PRT; 730 AA.
AC P34115;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cell surface glycoprotein GPI38A precursor.
GN FUSA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-32.
RC STRAIN-AX3;
RX MEDLINE=93193972; PubMed=7680629;
RA Fang H., Higa M., Suzuki K., Aliba K., Urushihara H., Yanagisawa K.;
RT "Molecular cloning and characterization of two genes encoding gpl38,
a cell surface glycoprotein involved in the sexual cell fusion of
Dictyostelium discoideum.";
RL Dev. Biol. 156:201-208(1993).
CC -!- FUNCTION: INVOLVED IN THE SEXUAL CELL FUSION OF D.DISCOIDEUM.
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
CC THAT CONTAINS A PHOSPHOCERAMIDE MOIETY.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE TIME OF ACQUISITION OF
CC FUSION COMPETENCE OF CELLS.
CC -!- PTM: THE SUGAR CHAINS MAY PLAY IMPORTANT ROLES IN CELL FUSION.
CC -!- MISCELLANEOUS: GPI38A EXPRESSION IS MUCH HIGHER THAN THAT OF
CC GPI38B AND MAY WELL BE THE MAJOR GENE FOR GPI38 PRODUCT.
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EMBL; D12883; BAA02287.1; -
PIR; A48832; A48832.
DictyDb; DD03014; fusa.
InterPro; IPR002909; IPT_TIG.
Pfam; PF01833; TIG; 1.
KW Glycoprotein; Signal; Multigene family; GPI-anchor; Repeat.
FT SIGNAL 1 20
FT CHAIN 21 708 CELL SURFACE GLYCOPROTEIN GPI38A.
FT PROPEP 709 730 REMOVED IN MATURE FORM (POTENTIAL).
FT LIPID 708 708 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 683 694 3 X 4 AA TANDEM REPEATS OF P-S-T-T.
FT REPEAT 683 686 1.
FT REPEAT 687 690 2.
FT REPEAT 691 694 3.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
```

FT	CARBOHYD	482	482	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	498	498	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	523	523	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	534	534	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	596	596	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	605	605	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	614	614	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	620	620	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	621	621	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	630	630	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	730 AA;	80960 MW;	C2BDB82BC24CD133	CRC64;
Query Match					
Best Local Similarity		72.5%;	Score 37;	DB 1;	Length 730;
Matches		6;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
QY	1 YYGDYEGY 8				
Db	343 YYNDYEQY 350				
RESULT 13					
GGT_BACSU					
ID	GGT_BACSU	STANDARD;	PRT;	587 AA.	
AC	P54422;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2).				
GN	GGT.				
OS	Bacillus subtilis.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1423;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=168 / JH642;				
RX	MEDLINE=96312380; PubMed=8763966;				
RA	Xu K., Strauch M.A.;				
RT	"Identification, sequence, and expression of the gene encoding gamma-glutamyltranspeptidase in Bacillus subtilis.";				
RT	glutamyltranspeptidase in Bacillus subtilis.";				
RL	J. Bacteriol. 178:4319-4322(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=168;				
RX	MEDLINE=98044033; PubMed=9384377;				
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;				

RT	"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";				
RT	Nature 390:249-256(1997).				
RN	[3]				
RP	SEQUENCE OF 36-52 AND 403-442, AND CHARACTERIZATION.				
RC	STRAIN=NR-1;				
RA	Ogawa Y., Hosoyama H., Hamano M., Motai H.;				
RT	"Purification and properties of gamma-glutamyltranspeptidase from Bacillus subtilis (natto).";				
RT	Agric. Biol. Chem. 55:2971-2977(1991).				
RL	-!- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid = peptide + 5-L-glutamyl-amino acid.				
CC	-!- ENZYME REGULATION: INHIBITED BY GLUCOSE.				
CC	-!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.				
CC	-!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE (BY SIMILARITY).				
CC	-!- SUBCELLULAR LOCATION: Secreted.				
CC	-!- DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF VEGETATIVE GROWTH.				
CC	-!- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.				
CC	-----				
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CC	-----				
DR	EMBL; U49358; AAC44233.1; -.				
DR	EMBL; Z99113; CAB13724.1; -.				
DR	EMBL; Z99114; CAB13734.1; -.				
DR	MEROPS; T03.001; -.				
DR	Subtilist; BGI1838; ggt.				
DR	InterPro; IPR000101; Gglutrnspptdase.				
DR	Pfam; PF01019; G_glu_transpept; 1.				
DR	PRINTS; PR01210; GGTRANSPASE.				
DR	TIGRFAMS; TIGR00066; g_glu_trans; 1.				
DR	PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.				
DR	Transferase; Acyltransferase; Signal; Glutathione biosynthesis; zymogen; Complete proteome.				
KW	SIGNAL	1	28	POTENTIAL.	
FT	CHAIN	29	402	GAMMA-GLUTAMYLTRANSPEPTIDASE LARGE CHAIN.	
FT	CHAIN	403	587	GAMMA-GLUTAMYLTRANSPEPTIDASE SMALL CHAIN.	
FT	BINDING	467	467	GAMMA-GLUTAMYL (POTENTIAL).	
FT	CONFLICT	46	46	D -> V (IN REF. 3).	
SQ	SEQUENCE	587 AA;	64189 MW;	6BF200CBA882C4F6	CRC64;
Query Match					
Best Local Similarity		70.6%;	Score 36;	DB 1;	Length 587;
Matches		5;	Conservative	2;	Mismatches 0; Indels 0; Gaps 0;
QY	2 YGDYEGY 8				
Db	:				
Db	277 WGDYQGY 283				
RESULT 14					
ACSA_RHOCA					
ID	ACSA_RHOCA	STANDARD;	PRT;	656 AA.	
AC	O68040;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-activating enzyme).				
GN	ACS.				
OS	Rhodobacter capsulatus (Rhodopseudomonas capsulata).				
OC	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;				
OC	Rhodobacter.				
OX	NCBI_TaxID=1061;				
RN	[1]				

```
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003 / St Louis;
RA MEDLINE=97404404; PubMed=9256491;
RX Vlcek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.;
RT "Sequence of a 189-kb segment of the chromosome of Rhodobacter
RT capsulatus SB1003."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
CC -!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
CC acetyl-CoA.
CC -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF010496; AAC16126.1; -.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase.
SQ SEQUENCE 656 AA; 72703 MW; 706EA969331D71C2 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 656;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YVGDYEGY 8
Db 495 YFGQYRGY 502
1:111111

RESULT 15
PERT_MOUSE 1
ID PERT_MOUSE STANDARD; PRT; 914 AA.
AC P35419;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thyroid peroxidase precursor (EC 1.11.1.8) (TPO).
GN TPO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thyroid;
RX MEDLINE=93154601; PubMed=7916704;
RA Kotani T., Umeki K., Yamamoto I., Takeuchi M., Takechi S.,
RA Nakayama T., Ohtaki S.;
RT "Nucleotide sequence of the cDNA encoding mouse thyroid peroxidase.";
RL Gene 128:289-290(1993).
CC -!- FUNCTION: IODINATION AND COUPLING OF THE HORMONAL TYROSINES
CC IN THYROGLOBULIN TO YIELD THE THYROID HORMONES T(3) AND T(4).
CC -!- CATALYTIC ACTIVITY: Iodide + H(2)O(2) = iodine + 2 H(2)O.
CC -!- COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.
CC -!- PATHWAY: Thyroid hormone biosynthesis.
CC -!- SUBCELLULAR LOCATION: Membrane.
CC -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. XPO SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; X60703; CAA43114.1; -.
DR PIR; JN0550; JN0550.
DR HSSP; P05164; 1CXP.
DR MGD; MGI:98813; Tpo.
DR InterPro; IPR002007; Anim_peroxidase.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF03098; An_peroxidase; 1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Transmembrane; Glycoprotein;
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 914 THYROID PEROXIDASE.
FT ACT_SITE 233 233 DISTAL HISTIDINE (POTENTIAL).
FT ACT_SITE 384 384 DISTAL ARGININE (POTENTIAL).
FT METAL 482 482 IRON (PROTOHEME IX AXIAL LIGAND) (BY
FT SIMILARITY).
FT TRANSMEM 835 859 POTENTIAL.
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 914 AA; 101342 MW; 595E9A0B71F3DD01 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 914;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YVGDYEGY 8
Db 454 YVGPYEGY 461
11111111
```

Search completed: December 23, 2002, 07:26:05
Job time : 3.7907 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 3.31783 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	80.4	435	16 Q9PN04	Q9pn04 campylobact
2	40	78.4	409	10 Q9LEB4	Q9leb4 nicotiana p
3	40	78.4	1650	5 O77328	O77328 plasmodium
4	39	76.5	1881	17 Q8TJS7	Q8tjs7 methanosarc
5	38	74.5	387	10 Q9FPJ8	Q9fpj8 arabidopsi
6	38	74.5	390	10 Q9FFU0	Q9ffu0 arabidopsi
7	38	74.5	595	16 O67245	O67245 aquifex aeo
8	38	74.5	660	16 Q9KGK8	Q9kgk8 bacillus ha
9	38	74.5	3216	16 Q98QZ9	Q98qz9 mycoplasma
10	37	72.5	89	5 O62093	O62093 caenorhabdi
11	37	72.5	104	5 Q9U601	Q9u601 anisakis si
12	37	72.5	154	17 O27163	O27163 methanobact
13	37	72.5	248	5 Q9W0H1	Q9w0h1 drosophila
14	37	72.5	279	4 Q9HAF2	Q9haf2 homo sapien
15	37	72.5	294	2 Q8VVN1	Q8vvnl vibrio chol
16	37	72.5	300	5 Q9W098	Q9w098 drosophila

17	37	72.5	376	4 Q9H7I9	Q9h7i9 homo sapien
18	37	72.5	394	17 Q8TNY5	Q8tny5 methanosarc
19	37	72.5	542	16 Q9JZ89	Q9jz89 neisseria m
20	37	72.5	542	16 Q9JUB3	Q9jub3 neisseria m
21	37	72.5	564	5 Q23118	Q23118 caenorhabdi
22	37	72.5	601	11 Q99KG1	Q99kg1 mus musculu
23	37	72.5	620	17 Q96XC8	Q96xc8 sulfolobus
24	37	72.5	632	11 Q8VHM5	Q8vhm5 mus musculu
25	37	72.5	636	4 Q9BV64	Q9bv64 homo sapien
26	37	72.5	1657	5 P90761	P90761 caenorhabdi
27	36	70.6	191	16 Q92CQ8	Q92cq8 listeria in
28	36	70.6	191	16 Q8Y7X0	Q8y7x0 listeria mo
29	36	70.6	252	16 Q97S13	Q97sl3 streptococc
30	36	70.6	299	17 Q8TL35	Q8tl35 methanosarc
31	36	70.6	307	5 Q9V5P1	Q9v5p1 drosophila
32	36	70.6	307	17 Q8TTD1	Q8tttd1 methanosarc
33	36	70.6	335	5 Q8SZN5	Q8szn5 drosophila
34	36	70.6	335	5 Q8SYP0	Q8syp0 drosophila
35	36	70.6	441	10 Q9LX71	Q9lxl71 arabidopsis
36	36	70.6	565	16 Q98RF4	Q98rf4 mycoplasma
37	36	70.6	605	17 Q8U130	Q8ul30 pyrococcus
38	36	70.6	618	10 Q9LWD5	Q9lwd5 oryza sativ
39	36	70.6	666	2 Q9RIK7	Q9rik7 thermotoga
40	36	70.6	669	16 Q9X0V4	Q9x0v4 thermotoga
41	36	70.6	680	2 Q9RIK9	Q9rik9 thermotoga
42	36	70.6	686	5 Q96453	Q96453 anopheles s
43	36	70.6	687	5 Q96753	Q96753 anopheles g
44	36	70.6	694	2 Q9Z187	Q9zi87 bacillus st
45	36	70.6	760	4 Q8TCI9	Q8tcic9 homo sapien

ALIGNMENTS

RESULT 1
Q9PN04
ID Q9PN04 PRELIMINARY; PRT; 435 AA.
AC Q9PN04;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein Cj1295.
GN Cj1295.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139078; CAB73722.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 435 AA; 49948 MW; 1DFD6DDD270C0877 CRC64;

Query Match 80.4%; Score 41; DB 16; Length 435;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGDYEGY 8
| | | | |
Db 325 YGDYDGY 331

RESULT 2

Q9LEB4 ID Q9LEB4 PRELIMINARY; PRT; 409 AA.
AC Q9LEB4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RNA binding protein 45.
GN RBP45.
OS Nicotiana glumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20555308; PubMed=11105760;
RA Lorkovic Z.J., Wiczorek Kirk D.A., Klahre U., Hemmings-Mieszcza M.,
RA Filipowicz W.;
RT "RBP45 and RBP47, two oligouridylylate-specific hnRNP-like proteins
interacting with poly(A)+ RNA in nuclei of plant cells.";
RL RNA 6:1610-1624(2000).
DR EMBL; AJ252767; CAC01237.1; -.
DR HSSP; P11940; IGVJ.
DR ANU-2DPAGE; Q9LEB4; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 409 AA; 45243 MW; 145EE701A89AF01D CRC64;

Query Match 78.4%; Score 40; DB 10; Length 409;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8
Db 394 YYGNYPGY 401

RESULT 3
O77328 ID O77328 PRELIMINARY; PRT; 1650 AA.
AC O77328;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative serine/threonine protein kinase.
GN PFC03856; MAL3P3.12.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum";
RL Nature 400:532-538(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z98547; CAB11112.2; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.

DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1650 AA; 193755 MW; D70FE19C5C640B5A CRC64;

Query Match 78.4%; Score 40; DB 5; Length 1650;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8
Db 525 YFDDYEGY 532

RESULT 4
Q8TJS7 ID Q8TJS7 PRELIMINARY; PRT; 1881 AA.
AC Q8TJS7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cell surface protein.
GN MA3700.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011081; AAM07055.1; -.
KW Complete proteome.
SQ SEQUENCE 1881 AA; 201366 MW; 836514E38E842A49 CRC64;

Query Match 76.5%; Score 39; DB 17; Length 1881;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8
Db 165 HYGDYVGY 172

RESULT 5
Q9FPJ8 ID Q9FPJ8 PRELIMINARY; PRT; 387 AA.
AC Q9FPJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AT5G54900.
GN AT5G54900/MBG8_17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Query Match 74.5%; Score 38; DB 16; Length 660;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| | | | |
Db 121 YLGDYEGW 128

RESULT 9

Q98QZ9 PRELIMINARY; PRT; 3216 AA.
AC Q98QZ9;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Hypothetical protein MYPV_2110.
GN MYPV_2110
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL045563; CAC13384.1; --
DR Mypulists; MYPV_2110; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 3216 AA; 359419 MW; A62ED95756BDB90C CRC64;

Query Match 74.5%; Score 38; DB 16; Length 3216;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| | | | |
Db 1978 YVDYEGF 1985

RESULT 10

O62093 PRELIMINARY; PRT; 89 AA.
AC O62093;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C37A5.8 protein.
GN C37A5.8
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92828; CAB07335.1; --
SQ SEQUENCE 89 AA; 10003 MW; C887044842E59E25 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 89;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| | | | |
Db 61 YGGYGGY 68

RESULT 11

Q9U601 PRELIMINARY; PRT; 104 AA.
AC Q9U601;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 11.5 kDa protein.
GN IAA99-ASL3-15A.
OS Anisakis simplex.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Anisakidae; Anisakis.
OX NCBI_TaxID=6269;
RN [1]
RP SEQUENCE FROM N.A.
RA Arrieta I., Del Barrio M., Vidarte L., Del Pozo V., Pastor C.,
RA Gonzalez-Cabrero J., Cardaba B., Rojo M., Minguez A., Corteano I.,
RA Gallardo S., Aceituno E., Palomino P., Lahoz C.;
RT "Anisakis simplex for a 12 kDa protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250043; CAB58174.1; --
KW Hypothetical protein.
SQ SEQUENCE 104 AA; 11456 MW; 419710152ADD6FAA CRC64;

Query Match 72.5%; Score 37; DB 5; Length 104;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
| | | | |
Db 63 YGGYGGY 70

RESULT 12

O27163 PRELIMINARY; PRT; 154 AA.
AC O27163;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Conserved protein.
GN MTH1091.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000879; AAB85580.1; --
DR InterPro; IPR002743; DUF57.
DR Pfam; PF01881; DUF57; 1.
DR ProDom; PD008324; DUF57; 1.

KW Complete proteome.
SQ SEQUENCE 154 AA; 18541 MW; 9EA3B9F89F7DE210 CRC64;

Query Match 72.5%; Score 37; DB 17; Length 154;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEG 7
:||||:|
Db 81 FYGDYDG 87

RESULT 13
Q9W0H1 PRELIMINARY; PRT; 248 AA.
AC Q9W0H1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG9184 protein.
GN CG9184.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003471; AAF47476.1; -.
DR FlyBase; FBgn0035208; CG9184.
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENS.
SQ SEQUENCE 248 AA; 26964 MW; 59CE24C83A55A3CD CRC64;

Query Match 72.5%; Score 37; DB 5; Length 248;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 160 YGGYGGY 167

RESULT 14
Q9HAF2 PRELIMINARY; PRT; 279 AA.
AC Q9HAF2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 30.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK021791; BAB13897.1; -.
DR InterPro; IPR004567; PanK_eukar.
DR Pfam; PF03630; Fumble; 1.
SQ SEQUENCE 279 AA; 30651 MW; AAD5DA42C94AEA3C CRC64;

Query Match 72.5%; Score 37; DB 4; Length 279;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
|||||
Db 163 YGGDYEGF 170

RESULT 15
Q8VVN1 PRELIMINARY; PRT; 294 AA.
AC Q8VVN1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 33.0 kDa protein.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MO10; TRANSPOSON-SXT ELEMENT;
RX MEDLINE=21485931; PubMed=11600347;
RA Hochhut B., Lotfi Y., Mazel D., Faruque S.M., Woodgate R.,
RA Waldor M.K.;
RT "Molecular Analysis of Antibiotic Resistance Gene Clusters in Vibrio
RT cholerae O139 and O1 SXT Constns.";
RL Antimicrob. Agents Chemother. 45:2991-3000(2001).
DR EMBL; AY034138; AAK64586.1; -.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 33023 MW; A0A2FA4C0173018F CRC64;

Query Match 72.5%; Score 37; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDYEGY 8
| | | | |
Db 74 GDYEGY 79

Search completed: December 23, 2002, 07:29:47
Job time : 6.31783 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 5.36822 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	10	AAW27424	CDR1 from light ch
2	48	100.0	10	AAW73169	CDR1 of light chai
3	48	100.0	10	AAZ28390	Peptide fragment f
4	48	100.0	10	AAZ97232	Complementary dete
5	48	100.0	10	AAZ77582	Anti-human VEGF re
6	48	100.0	10	AAZ77588	Anti-human VEGF re
7	48	100.0	10	AAE13140	Humanised antibody
8	48	100.0	10	AAZ82706	VEGF antagonist an
9	48	100.0	10	AAZ83163	Mouse ganglioside
10	48	100.0	10	AAZ78851	Anti-human Flt-1 a

11	48	100.0	10	AAZ78857	Anti-human Flt-1 a
12	48	100.0	10	AAU74409	Light chain comple
13	48	100.0	10	AAU70361	Mouse Kappa VI lig
14	48	100.0	96	AAU08982	Single-chain antib
15	48	100.0	99	AAU08981	Single-chain antib
16	48	100.0	102	AAZ07321	VK domain of antib
17	48	100.0	102	AAW14489	Monoclonal antibod
18	48	100.0	102	AAZ99872	Monoclonal antibod
19	48	100.0	103	AAZ26002	L-chain variable r
20	48	100.0	105	AAW03182	Guy's 13 anti-Stre
21	48	100.0	106	AAE13144	Humanised antibody
22	48	100.0	106	AAU74418	Antigen-binding pr
23	48	100.0	107	AAZ83159	Mouse ganglioside
24	48	100.0	107	AAZ83167	Ganglioside GM2 an
25	48	100.0	108	AAZ21293	Murine VL kappa gr
26	48	100.0	108	AAZ21301	Murine VL kappa gr
27	48	100.0	108	AAZ21303	Murine VL kappa gr
28	48	100.0	108	AAZ79884	Anti-EGFR antibody
29	48	100.0	108	AAZ97236	Variable light cha
30	48	100.0	108	AAZ82710	VEGF antagonist an
31	48	100.0	108	AAU74413	Antigen-binding pr
32	48	100.0	110	AAZ21846	Light chain variab
33	48	100.0	113	AAZ48936	Anti-TrkA murine m
34	48	100.0	125	AAE13146	Chimeric p1C11 lig
35	48	100.0	125	AAZ82702	VEGF antagonist an
36	48	100.0	126	AAZ77594	Anti-human VEGF re
37	48	100.0	126	AAZ77598	Anti-human VEGF re
38	48	100.0	126	AAZ77599	Anti-human VEGF re
39	48	100.0	126	AAZ77601	Anti-human VEGF re
40	48	100.0	126	AAZ78863	Anti-human Flt-1 m
41	48	100.0	126	AAZ78867	Anti-human Flt-1 a
42	48	100.0	126	AAZ78868	Anti-human Flt-1 a
43	48	100.0	126	AAZ78870	Anti-human Flt-1 a
44	48	100.0	128	AAZ77592	Anti-human VEGF re
45	48	100.0	128	AAZ77597	Anti-human VEGF re

ALIGNMENTS

RESULT 1	
AAW27424	
ID	AAW27424 standard; peptide; 10 AA.
XX	
AC	AAW27424;
XX	
DT	19-DEC-1997 (first entry)
XX	
DE	CDR1 from light chain variable region of KML486 antibody.
XX	
KW	Complementarity determining region; CDR; light chain; treatment;
KW	variable region; murine; mouse; human; interleukin 5; IL-5;
KW	receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW	assay; diagnosis; allergic respiratory disease; chronic bronchitis;
OS	Mus spp.
XX	
PN	WO9710354-A1.
PD	20-MAR-1997.
XX	
PF	11-SEP-1996; 96WO-JP02588.
XX	
PR	11-SEP-1995; 95JP-0232384.
XX	
PA	(KYOW) KYOWA HAKKO KOGYO KK.
XX	
PI	Anazawa H, Furuya A, Hanai N, Iida A, Koike M;
PI	Nakamura K, Takatsu K;
XX	
DR	WPI; 1997-202249/18.
XX	
PT	Antibody against alpha-chain of human interleukin 5 receptor -

PT useful for diagnosis and treatment of respiratory allergic diseases,
PT e.g. chronic bronchitis
XX
PS Claim 10; Page 165; 238pp; Japanese.
XX
CC The present sequence is complementarity determining region 1 (CDR1)
CC from the light chain variable region of the murine anti-human
CC interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal
CC antibody (MAB) KM1486. KM1486 is produced by the hybridoma
CC FERM BP-5651, which was prepared by immunising Balb/c mice with
CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
CC myeloma P3-U1 cells and screening the resultant hybridomas. The MAb
CC can be used to detect or assay for hIL-5R alpha and cells
CC expressing it on their surface, especially to diagnose allergic
CC respiratory diseases, e.g. chronic bronchitis. It can also be used
CC to treat such diseases.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db |||||
1 SASSSSVSYMH 10

RESULT 2
AAW73169 standard; peptide; 10 AA.
XX
AC AAW73169;
XX
DT 22-JAN-1999 (first entry)
XX
DE CDR1 of light chain of ganglioside GM2 targeting antibody.
XX
KW Ganglioside GM2; antibody; complementarity determining region; cancer;
KW anti-tumour agent.
XX
OS Homo sapiens.
XX
PN JP10257893-A.
XX
PD 29-SEP-1998.
XX
PF 19-MAR-1997; 97JP-0066981.
XX
PR 19-MAR-1997; 97JP-0066981.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
DR WPI; 1998-575904/49.
XX
PT A human type complementarity determining region transplanted
PT antibody against ganglioside GM2 - useful as an anti-tumour agent
PT and as a diagnostic for related cancers
XX
PS Claim 1; Page 29; 66pp; Japanese.
XX
CC This sequence represents a complementarity determining region (CDR) from
CC the heavy chain of the antibody of the invention. The antibody of the
CC invention is a human CDR transplanted antibody that reacts specifically
CC with ganglioside GM2. DNA encoding the antibody, and vectors and
CC transformants containing it, can be used for the recombinant production
CC of the antibody. The antibody itself can be used as an anti-tumour agent
CC or as a diagnostic tool for related cancers. The antibody has antitumour
CC activity against ganglioside GM2 positive cells.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db |||||
1 SASSSSVSYMH 10

RESULT 3
AAW28390 standard; protein; 10 AA.
ID AAY28390
XX
AC AAY28390;
XX
DT 04-NOV-1999 (first entry)
XX
DE Peptide fragment from the human anti-GM2 light chain in REI.
XX
KW antibody; REI; complementarity determining region; CDR;
KW chimeric; light chain; heavy chain.
XX
OS Homo sapiens.
XX
PN US5939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-0483528.
XX
PR 07-JUN-1995; 95US-0483528.
PR 07-SEP-1993; 93US-0116778.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
XX
DR WPI; 1999-468416/39.
XX
PT Chimeric human antibody expression vectors
XX
PS Example 2; Column 157; 188pp; English.
XX
CC The sequences AAY28390 to AAY28392 replace the CDR regions of the NEWM
CC DNA and they produce AAY28394, the hKM796L human anti-GM2 antibody light
CC chain.
CC Chimeric human antibodies of the invention are useful in the treatment
CC of cancer, especially that which is of neural ectodermal origin.
CC In contrast to prior art constructs based on mouse monoclonal
CC antibodies, the chimeric human antibodies do not cause anti-mouse
CC immunoglobulin production.
CC The chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal
CC antibodies.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db |||||
1 SASSSSVSYMH 10

RESULT 4
AAW97232 standard; protein; 10 AA.
ID AAY97232
XX
AC AAY97232;
XX
DT 19-DEC-2000 (first entry)

DR WPI; 2000-072431/06.
XX Gene recombinant antibodies, useful for diagnosis and as remedies for
PT diseases due to abnormal neovascularization e.g. proliferation or
PT metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
PT and psoriasis
XX
PS Claim 10; Page 161; 210pp; Japanese.
XX
CC The invention relates to a gene recombinant antibody that has specific
CC reaction with human vascular endothelial growth factor (VEGF) receptor
CC Flt-1. The antibodies are useful for diagnosis and as remedies for
CC diseases due to abnormal neovascularisation such as proliferation or
CC metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
CC retinopathy, premature retinopathy and psoriasis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 1 SASSSSVSYMH 10

RESULT 7
AAE13140
ID AAE13140 standard; peptide; 10 AA.
XX
AC AAE13140
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody murine light chain hypervariable region (VL) CDR1.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytosolic; light chain hypervariable region; VL; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-1; CDR-1; mouse.
XX
OS Mus sp.
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafii S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21666.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 14; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region

CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody murine light chain hypervariable region (VL) CDR-1 used in the
CC exemplification of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 1 SASSSSVSYMH 10

RESULT 8
AAB82706
ID AAB82706 standard; Peptide; 10 AA.
XX
AC AAB82706;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 VL CDR-1.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; angiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
KW complementarity determining region.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
PS Disclosure; Page 37; 42pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 1 of the light chain variable region (see also AAB82702) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a

CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db | | | | | | | | | |
1 SASSSVSVMH 10

RESULT 9
AAB83163
ID AAB83163 standard; peptide; 10 AA.
XX
AC AAB83163;
XX
DT 02-JUL-2001 (first entry)
XX
DE Mouse ganglioside GM2 antibody light chain variable region CDR1.
XX
KW Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer;
KW complementarity determining region; CDR.
XX
OS Mus sp.
XX
PN WO200123431-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP06775.
XX
PR 30-SEP-1999; 99JP-0278292.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Nakamura K, Niwa R;
XX
XX WPI; 2001-266142/27.
XX
PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
PT radioisotopes or proteins for treatment and diagnosis of cancer -
XX
PS Claim 4; Page 71; 80pp; Japanese.
XX
CC The present invention relates to derivatives of an antibody against
CC ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope,
CC protein or small drug in the treatment and diagnosis of cancer.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db | | | | | | | | | |
1 SASSSVSVMH 10

RESULT 10

AAB78851
ID AAB78851 standard; Peptide; 10 AA.
XX
AC AAB78851;
XX
DT 20-APR-2001 (first entry)
XX
DE Anti-human Flt-1 antibody KM1732 L chain V region CDR 1 peptide.
XX
KW Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
KW delayed hypersensitivity; malignant tumour; arteriosclerosis.
XX
OS Mus musculus.
XX
PN WO200079275-A1.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-JP03957.
XX
PR 17-JUN-1999; 99JP-0171709.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Shibuya M;
XX
DR WPI; 2001-080847/09.
XX
PT Substances binding to human vascular endothelial growth factor receptor
PT Flt-1, used for diagnosis and treatment of inflammatory diseases,
PT arteriosclerosis, cancer and delayed hypersensitivity -
XX
PS Example 3; Page 127; 164pp; Japanese.
XX
CC This invention relates to a reagent for detecting differentiation of
CC monocytes and macrophages from haematopoietic stem cells, containing a
CC substance which binds to human vascular endothelial growth factor (VEGF)
CC receptor Flt-1. The invention also includes a method for diagnosing a
CC disease in which the differentiation of monocytes and macrophages is
CC implicated, using the reagent, and an agent for the treatment of diseases
CC diagnosed using the method, containing a substance which binds to Flt-1
CC or a substance which inhibits the signal transduction of Flt-1. Diseases
CC which may be diagnosed or treated include inflammation, delayed
CC hypersensitivity, malignant tumours and arteriosclerosis.
CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences
CC encoding anti-human Flt-1 monoclonal antibody fragments, and
CC oligonucleotides used in the construction of the antibody. The monoclonal
CC antibody is used in the reagent of the invention. PCR primers AAF70245 -
CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody
CC DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments
CC of the anti-human Flt-1 antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db | | | | | | | | | |
1 SASSSVSVMH 10

RESULT 11
AAB78857
ID AAB78857 standard; Peptide; 10 AA.
XX
AC AAB78857;
XX
DT 20-APR-2001 (first entry)
XX
DE Anti-human Flt-1 antibody KM1750 L chain V region CDR 1 peptide.

XX Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
KW delayed hypersensitivity; malignant tumour; arteriosclerosis.
XX
OS Mus musculus.
XX
PN WO200079275-A1.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-JP03957.
XX
PR 17-JUN-1999; 99JP-0171709.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Shibuya M;
XX
DR WPI; 2001-080847/09.
XX
PT Substances binding to human vascular endothelial growth factor receptor
PT Flt-1, used for diagnosis and treatment of inflammatory diseases,
PT arteriosclerosis, cancer and delayed hypersensitivity -
XX
PS Example 3; Page 128; 164pp; Japanese.
XX
CC This invention relates to a reagent for detecting differentiation of
CC monocytes and macrophages from haematopoietic stem cells, containing a
CC substance which binds to human vascular endothelial growth factor (VEGF)
CC receptor Flt-1. The invention also includes a method for diagnosing a
CC disease in which the differentiation of monocytes and macrophages is
CC implicated, using the reagent, and an agent for the treatment of diseases
CC diagnosed using the method, containing a substance which binds to Flt-1
CC or a substance which inhibits the signal transduction of Flt-1. Diseases
CC which may be diagnosed or treated include inflammation, delayed
CC hypersensitivity, malignant tumours and arteriosclerosis.
CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences
CC encoding anti-human Flt-1 monoclonal antibody fragments, and
CC oligonucleotides used in the construction of the antibody. The monoclonal
CC antibody is used in the reagent of the invention. PCR primers AAF70245 -
CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody
CC DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments
CC of the anti-human Flt-1 antibody.

XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 48; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | |
Db 1 SASSSVSYMH 10

RESULT 12
AAU74409
ID AAU74409 standard; peptide; 10 AA.
XX
AC AAU74409;
XX
DT 26-MAR-2002 (first entry)
XX
DE Light chain complementarity determining region L1 (CDRL1).

XX Complementarity determining region; CDR; CDRL1; antigen; cytostatic;
KW anglogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody light chain variable domain.
XX
OS Mus sp

PN WO200190192-A2.

XX 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US16924.

PR 24-MAY-2000; 2000US-206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

XX WPI; 2002-106189/14.

DR N-PSDB; AAS20280.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 55; Page 56; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the light chain variable domain
CC complementarity determining region L1 (CDRL1) incorporated into an
CC antigen-binding protein described in the method of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 48; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | |
Db 1 SASSSVSYMH 10

RESULT 13
AAU70361
ID AAU70361 standard; Peptide; 10 AA.
XX
AC AAU70361;
XX
DT 14-FEB-2002 (first entry)
XX
DE Mouse Kappa VI light chain CDR1.

XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array;
KW IgM; IgG; IgA; IgD; IgE; IgM; kappa; lambda; CHBP.
XX
OS Mus musculus.

XX WO200183806-A1.

XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US14349.
XX PR 02-MAY-2000; 2000US-0563222.
XX PA (EPIC-) EPICYTE PHARM INC.
XX PI Hiatt AC, Hein MB;
XX DR WPI; 2002-055482/07.
XX
XX PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array -
XX
XX PS Disclosure; Page 14; 129pp; English.
XX
XX CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that
CC binds to a ligand, and transformed plant cells are selected, and
CC preparing an IgBP array in plant cells. At least one peptide sequence has
CC at least 75% sequence identity to a framework region (FR) of a native
CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
CC The method is useful for preparing an immunoglobulin binding protein
CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
CC desired characteristics. The present sequence is a mammalian
CC immunoglobulin derived peptide that may be incorporated into an IgBP of
CC the invention.
XX
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 1 SASSSVSYMH 10

RESULT 14
AAU08982
ID AAU08982 standard; protein; 96 AA.
XX AC AAU08982;
XX DT 18-DEC-2001 (first entry)
XX DE Single-chain antibody scFvA7 light chain.
XX KW Antibody; scFvA7; light chain; angiogenesis; vascularisation;
KW vascular endothelial; growth factor receptor 2; VEGFR-2; carcinoma.
XX OS Mus sp.
OS Synthetic.
XX PN EP1130032-A1.
XX PD 05-SEP-2001.
XX PF 28-FEB-2000; 2000EP-0104082.
XX PR 28-FEB-2000; 2000EP-0104082.
XX

PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX PI Boeldicke T, Welch H, Tesar M, Yayon A;
XX DR WPI; 2001-591521/67.
XX
XX PT Single-chain antibody that recognizes human vascular endothelial growth
PT factor receptor-2 is useful as a marker for angiogenesis or
PT vascularisation in human tissues and for cell sorting of vascular
PT endothelial cells -
XX
XX PS Claim 1; Page 20; 35pp; English.
XX
XX CC The invention relates to novel single-chain antibody recognizing human
CC vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a
CC polypeptide having variable heavy (VH) and variable light (VL) domains
CC connected by a linker, and their allelic variants and mutants. The
CC antibody is useful as an immunohistochemical marker for angiogenesis
CC or vascularisation in a human tissue from cryosection or a growing
CC carcinoma, for vascular and stem cell targeting a drug or toxin,
CC radionuclide, gene or viral coat protein conjugated to it, for
CC fluorescence activated cell sorting (FACS) analysis and sorting of
CC cells expressing human vascular endothelial growth factor receptor-2,
CC such as human vascular endothelial cells, human megakaryocytes and
CC their progenitor cells, human haematopoietic stem cells from bone
CC marrow, umbilical cord blood or mobilised peripheral blood on their
CC surfaces. Recombinant single chain antibodies have many advantages
CC compared to monoclonal antibodies derived from hybridomas. The
CC recombinant antibodies are more easily expressed and prepared in
CC bacteria, easily purified from the bacteria periplasm or supernatant
CC without risk of contamination with serum-components. No expensive
CC cell-culture medium and expensive cell-culture laboratory is needed and
CC they are prepared by economical and cheap method. Because of the small
CC size they penetrate better into cells and tissue and are better used
CC for in vivo imaging and in vivo diagnostic applications. The
CC single-chain antibodies are easily fused to a drug, toxin,
CC radionuclide, gene or a viral coat protein. The present sequence is
CC the variable light chain of antibody scFvA7.
XX
XX SQ Sequence 96 AA;

Query Match 100.0%; Score 48; DB 22; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 16 SASSSVSYMH 25

RESULT 15
AAU08981
ID AAU08981 standard; protein; 99 AA.
XX AC AAU08981;
XX DT 18-DEC-2001 (first entry)
XX DE Single-chain antibody scFvA2 light chain.
XX KW Antibody; scFvA7; light chain; angiogenesis; vascularisation;
KW vascular endothelial; growth factor receptor 2; VEGFR-2; carcinoma.
XX OS Mus sp.
OS Synthetic.
XX PN EP1130032-A1.
XX PD 05-SEP-2001.
XX PF 28-FEB-2000; 2000EP-0104082.
XX PR 28-FEB-2000; 2000EP-0104082.

XX PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX PI Boeldicke T, Weich H, Tesar M, Yavon A;
XX DR WPI; 2001-591521/67.
XX PT Single-chain antibody that recognizes human vascular endothelial growth
PT factor receptor-2 is useful as a marker for angiogenesis or
PT vascularisation in human tissues and for cell sorting of vascular
PT endothelial cells -
XX PS Claim 1; Page 20; 35pp; English.
XX CC The invention relates to novel single-chain antibody recognizing human
CC vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a
CC polypeptide having variable heavy (VH) and variable light (VL) domains
CC connected by a linker, and their allelic variants and mutants. The
CC antibody is useful as an immunohistochemical marker for angiogenesis
CC or vascularisation in a human tissue from cryosection or a growing
CC carcinoma, for vascular and stem cell targeting a drug or toxin,
CC radionuclide, gene or viral coat protein conjugated to it, for
CC fluorescence activated cell sorting (FACS) analysis and sorting of
CC cells expressing human vascular endothelial growth factor receptor-2,
CC such as human vascular endothelial cells, human megakaryocytes and
CC their progenitor cells, human haematopoietic stem cells from bone
CC marrow, umbilical cord blood or mobilised peripheral blood on their
CC surfaces. Recombinant single chain antibodies have many advantages
CC compared to monoclonal antibodies derived from hybridomas. The
CC recombinant antibodies are more easily expressed and prepared in
CC bacteria, easily purified from the bacteria periplasm or supernatant
CC without risk of contamination with serum-components. No expensive
CC cell-culture medium and expensive cell-culture laboratory is needed and
CC they are prepared by economical and cheap method. Because of the small
CC size they penetrate better into cells and tissue and are better used
CC for in vivo imaging and in vivo diagnostic applications. The
CC single-chain antibodies are easily fused to a drug, toxin,
CC radionuclide, gene or a viral coat protein. The present sequence is
CC the variable light chain of antibody scFvA2.
XX SQ Sequence 99 AA;

Query Match 100.0%; Score 48; DB 22; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASSSVSVMH 10
Db 16 SASSSVSVMH 25

Search completed: December 23, 2002, 07:25:05
Job time : 6.36822 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 0.930233 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	10 US-09-976-787-4	Sequence 4, Appli
2	48	100.0	10	10 US-09-865-198-4	Sequence 4, Appli
3	48	100.0	105	9 US-09-982-107-12	Sequence 12, Appl
4	48	100.0	106	10 US-09-976-787-24	Sequence 24, Appl
5	48	100.0	106	10 US-09-865-198-23	Sequence 23, Appl
6	48	100.0	107	9 US-09-144-886-76	Sequence 76, Appl
7	48	100.0	107	9 US-09-144-886-82	Sequence 82, Appl
8	48	100.0	107	9 US-09-144-886-83	Sequence 83, Appl
9	48	100.0	107	9 US-09-144-886-88	Sequence 88, Appl
10	48	100.0	108	10 US-09-976-787-8	Sequence 8, Appli
11	48	100.0	108	10 US-09-865-198-8	Sequence 8, Appli
12	48	100.0	238	10 US-09-976-787-29	Sequence 29, Appl
13	48	100.0	238	10 US-09-865-198-28	Sequence 28, Appl
14	48	100.0	240	10 US-09-976-787-28	Sequence 28, Appl
15	48	100.0	240	10 US-09-865-198-27	Sequence 27, Appl
16	47	97.9	119	10 US-09-808-037-28	Sequence 28, Appl
17	47	97.9	239	10 US-09-808-037-6	Sequence 6, Appli
18	45	93.8	10	10 US-09-910-059-26	Sequence 26, Appl
19	45	93.8	107	10 US-09-910-059-50	Sequence 50, Appl

20	45	93.8	107	10	US-09-910-059-61	Sequence 61, Appl
21	45	93.8	107	10	US-09-910-059-65	Sequence 65, Appl
22	45	93.8	107	10	US-09-910-059-71	Sequence 71, Appl
23	45	93.8	108	10	US-09-910-059-9	Sequence 9, Appli
24	45	93.8	235	10	US-09-910-059-17	Sequence 17, Appl
25	45	93.8	235	10	US-09-910-059-52	Sequence 52, Appl
26	45	93.8	235	10	US-09-910-059-97	Sequence 97, Appl
27	45	93.8	235	10	US-09-910-059-99	Sequence 99, Appl
28	44	91.7	10	9	US-09-771-415-3	Sequence 3, Appli
29	44	91.7	10	9	US-09-996-288-14	Sequence 14, Appl
30	44	91.7	10	10	US-09-796-848A-5	Sequence 5, Appli
31	44	91.7	106	9	US-09-771-415-1	Sequence 1, Appli
32	44	91.7	106	9	US-09-771-415-17	Sequence 17, Appl
33	44	91.7	106	9	US-09-771-415-19	Sequence 19, Appl
34	44	91.7	106	9	US-09-771-415-21	Sequence 21, Appl
35	44	91.7	106	9	US-09-771-415-23	Sequence 23, Appl
36	44	91.7	106	9	US-09-771-415-25	Sequence 25, Appl
37	44	91.7	106	9	US-09-996-288-13	Sequence 13, Appl
38	44	91.7	106	9	US-09-996-288-54	Sequence 54, Appl
39	44	91.7	106	9	US-09-996-288-56	Sequence 56, Appl
40	44	91.7	106	9	US-09-996-288-57	Sequence 57, Appl
41	44	91.7	106	9	US-09-996-288-59	Sequence 59, Appl
42	44	91.7	106	9	US-09-996-288-60	Sequence 60, Appl
43	44	91.7	106	9	US-09-996-288-62	Sequence 62, Appl
44	44	91.7	106	9	US-09-996-288-64	Sequence 64, Appl
45	44	91.7	106	9	US-09-996-288-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-4
; Sequence 4, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-4

Query Match 100.0%; Score 48; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 1 SASSSVSYMH 10

RESULT 2
US-09-865-198-4
; Sequence 4, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-4

Query Match 100.0%; Score 48; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAS\$SVSYMH 10
| | | | |
Db 1 SAS\$SVSYMH 10

RESULT 3
US-09-982-107-12
; Sequence 12, Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: CHIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12

Query Match 100.0%; Score 48; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAS\$SVSYMH 10
| | | | |
Db 24 SAS\$SVSYMH 33

RESULT 4
US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAS\$SVSYMH 10
| | | | |
Db 24 SAS\$SVSYMH 33

RESULT 5
US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAS\$SVSYMH 10
| | | | |
Db 24 SAS\$SVSYMH 33

RESULT 6
US-09-144-886-76
; Sequence 76, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C9 region VL epitope 1
US-09-144-886-76

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAS\$SVSYMH 10
| | | | |
Db 24 SAS\$SVSYMH 33

RESULT 7

US-09-144-886-82
; Sequence 82, Application US/091444886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1E8 region VL epitope 1
US-09-144-886-82

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 24 SASSSVSYMH 33

RESULT 8
US-09-144-886-83
; Sequence 83, Application US/091444886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1G7 region VL epitope 1
US-09-144-886-83

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 24 SASSSVSYMH 33

RESULT 9
US-09-144-886-88
; Sequence 88, Application US/091444886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO

; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/a clone
; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 24 SASSSVSYMH 33

RESULT 10
US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 24 SASSSVSYMH 33

RESULT 11
US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse

US-09-865-198-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 24 SASSSVSVMH 33

RESULT 12

US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US 09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 156 SASSSVSVMH 165

RESULT 13

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 156 SASSSVSVMH 165

RESULT 14

US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 156 SASSSVSVMH 165

RESULT 15

US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 156 SASSSVSVMH 165

Search completed: December 23, 2002, 07:58:18
Job time : 0.930233 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 1.97674 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	48	100.0	91	2	S17629	Ig kappa chain V r
2	48	100.0	91	2	S17637	Ig kappa chain V r
3	48	100.0	91	2	S17639	Ig kappa chain V r
4	48	100.0	94	2	S20650	Ig heavy chain V r
5	48	100.0	94	2	S20653	Ig heavy chain V r
6	48	100.0	97	2	S26341	Ig light chain V r
7	48	100.0	97	2	PH1084	Ig light chain V r
8	48	100.0	99	2	D38601	Ig kappa chain V r
9	48	100.0	100	2	S29590	Ig kappa chain V r
10	48	100.0	102	2	S11115	Ig kappa chain V r
11	48	100.0	102	2	S24214	Ig kappa chain V r
12	48	100.0	103	2	S29591	Ig kappa chain V r
13	48	100.0	104	2	B49049	Ig kappa chain V r
14	48	100.0	106	2	B54378	Ig light chain V r
15	48	100.0	106	2	PS0071	Ig kappa chain V r
16	48	100.0	106	2	PS0072	Ig kappa chain V r
17	48	100.0	106	2	S11114	Ig kappa chain V r
18	48	100.0	106	2	S11120	Ig kappa chain V r
19	48	100.0	107	1	KVMSX4	Ig kappa chain V r
20	48	100.0	107	2	A30562	Ig kappa chain V r
21	48	100.0	107	2	B30562	Ig kappa chain V r
22	48	100.0	107	2	PT0395	Ig light chain V r
23	48	100.0	107	2	PT0398	Ig light chain V r
24	48	100.0	107	2	PT0399	Ig light chain V r
25	48	100.0	107	2	PT0400	Ig light chain V r
26	48	100.0	107	2	PT0401	Ig light chain V r
27	48	100.0	107	2	PT0402	Ig light chain V r
28	48	100.0	107	2	PT0403	Ig light chain V r
29	48	100.0	107	2	S11112	Ig kappa chain V r

30 48 100.0 107 2 S11113 Ig kappa chain V r
31 48 100.0 107 2 S11116 Ig kappa chain V r
32 48 100.0 107 2 S11117 Ig kappa chain V r
33 48 100.0 107 2 S11118 Ig kappa chain V r
34 48 100.0 107 2 S11119 Ig kappa chain V r
35 48 100.0 107 2 S11121 Ig kappa chain V r
36 48 100.0 107 2 S11123 Ig kappa chain V r
37 48 100.0 107 2 PT0406 Ig kappa chain V r
38 48 100.0 108 2 G30560 Ig kappa chain pre
39 48 100.0 130 1 JL0079 Ig kappa chain pre
40 48 100.0 140 2 PL0013 Ig kappa chain V r
41 47 97.9 107 2 PD0011 Ig kappa chain V r
42 47 97.9 107 2 PC4405 Ig kappa chain V r
43 45 93.8 76 2 A48784 Ig kappa V regions
44 45 93.8 91 2 S17626 Ig kappa chain V r
45 44 91.7 91 2 S17628 Ig kappa chain V r

ALIGNMENTS

RESULT 1
S17629
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17629
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17629
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-91 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 16 SASSSVSYMH 25

RESULT 2
S17637
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17637
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17637
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-91 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 16 SASSSVSYMH 25

```

C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 6
S26341
Ig light chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26341; S78448
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26341
A;Molecule type: mRNA
A;Residues: 1-97 <STA>
A;Cross-references: EMBL:X59179
R;Caton, A.J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S78447
A;Accession: S78448
A;Molecule type: mRNA
A;Residues: 1-39,'R',41-97,'L' <CAT>
A;Cross-references: EMBL:X59179; NID:g52311; PIDN:CAA41889.1; PID:g1334060
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-84/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 19 SASSSVSYMH 28

RESULT 7
PH1084
Ig light chain V region (clone 202.61) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1084
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1084
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 5
S20653
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20653
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20653
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LOS>
A;Cross-references: EMBL:X65006; NID:g52645; PIDN:CAA46139.1; PID:g52646
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 4
S20650
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20650
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LOS>
A;Cross-references: EMBL:X65006; NID:g52645; PIDN:CAA46139.1; PID:g52646
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 16 SASSSVSYMH 25

RESULT 3
S17639
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17639
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17639
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-91 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 16 SASSSVSYMH 25

RESULT 4
S20650
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20650
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LOS>
A;Cross-references: EMBL:X65009; NID:g52651; PIDN:CAA46142.1; PID:g52652
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```

RESULT 8
D38601
Ig kappa chain V region (6A7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: D38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D38601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-99 <GOS>
A;Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 16 SASSSVSVMH 25

RESULT 9
S29590
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29590
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29590
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <KAV>
A;Cross-references: EMBL:X59093; NID:g52225; PIDN:CAA41819.1; PID:g52226
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 24 SASSSVSVMH 33

RESULT 10
S11115
Ig kappa chain V region (clone NQ2-20.5.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11115
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11115
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-102 <KAA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 24 SASSSVSVMH 33

RESULT 11
S24214
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24214
R;Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A;Title: Deletions of immunoglobulin C(kappa) region characterized by the circular ex
A;Reference number: S24214; MUID:91217618; PMID:1902500
A;Accession: S24214
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-102 <SHI>
A;Cross-references: EMBL:X58204
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-87/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 22 SASSSVSVMH 31

RESULT 12
S29591
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <KAV>
A;Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
|||||
Db 23 SASSSVSVMH 32

RESULT 13
B49049
Ig kappa chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR ant

A:Reference number: A49049; MUID:93049629; PMID:1425914
A:Accession: B49049
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-104 <ARM>
A:Experimental source: BALB/c
A:Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIP:118299)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
 |||||
Db 24 SASSSVSYMH 33

RESULT 14

B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B54378
R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
A:Reference number: A54378; MUID:94165109; PMID:7509814
A:Accession: B54378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <AGA>
A:Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A:Experimental source: spleen and myeloma cell line MOPC 315.43
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
 |||||
Db 24 SASSSVSYMH 33

RESULT 15

PS0071
Ig kappa chain V region (38C13.V8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0071
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 270, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0071
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
 |||||
Db 24 SASSSVSYMH 33

Search completed: December 23, 2002, 07:31:35
Job time : 1.97674 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 0.988372 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	107	1 KV6A_MOUSE	P01675 mus musculu
2	48	100.0	107	1 KV6B_MOUSE	P01676 mus musculu
3	48	100.0	107	1 KV6C_MOUSE	P01677 mus musculu
4	48	100.0	107	1 KV6D_MOUSE	P01678 mus musculu
5	48	100.0	107	1 KV6E_MOUSE	P04940 mus musculu
6	48	100.0	107	1 KV6F_MOUSE	P04941 mus musculu
7	48	100.0	107	1 KV6G_MOUSE	P04942 mus musculu
8	48	100.0	107	1 KV6H_MOUSE	P04943 mus musculu
9	48	100.0	107	1 KV6I_MOUSE	P04944 mus musculu
10	42	87.5	108	1 KV6J_MOUSE	P04945 mus musculu
11	36	75.0	107	1 KV6K_MOUSE	P01679 mus musculu
12	34	70.8	129	1 KV4A_MOUSE	P01680 mus musculu
13	34	70.8	270	1 ALYS_BPRT	Q38135 bacterioph
14	34	70.8	731	1 BGAL_MALDO	P48981 malus domes
15	33	68.8	271	1 RRF_SPIOL	P82231 spinacia ol
16	33	68.8	405	1 CBG_HUMAN	P08185 homo sapien
17	32	66.7	394	1 DUS4_HUMAN	Q13115 homo sapien
18	32	66.7	933	1 SLAP_CAMFE	P35827 campylobact
19	31	64.6	230	1 YLME_BACSU	O31727 bacillus su
20	31	64.6	318	1 ATH4_ARATH	P92953 arabidopsis
21	31	64.6	377	1 Y835_METJA	Q58245 methanococc
22	31	64.6	460	1 MVIN_HELPJ	O92kw7 helicobacte
23	31	64.6	461	1 MVIN_HELPY	O25551 helicobacte
24	31	64.6	989	1 PTP3_DICDI	P54637 dictyosteli
25	31	64.6	1380	1 ZMS1_YEAST	P46974 saccharomyc
26	31	64.6	1520	1 PMPD_CHLMU	Q9plb0 chlamydia m
27	30	62.5	218	1 NUKM_ARATH	O42577 arabidopsis
28	30	62.5	367	1 CCR3_MOUSE	O88410 mus musculu
29	30	62.5	368	1 CCR3_HUMAN	P49682 homo sapien
30	30	62.5	383	1 CBG_RABIT	P23775 oryctolagus
31	30	62.5	418	1 HLT_VIBPA	Q99289 vibrio para
32	30	62.5	435	1 FUT9_ARATH	Q9xi77 arabidopsis
33	30	62.5	447	1 COBB_METTH	O27509 methanobact

34	30	62.5	448	1 FADL_ECOLI	P10384 escherichia
35	30	62.5	461	1 NORM_VIBCH	Q9kru4 vibrio chol
36	30	62.5	481	1 HH_DROHY	P56674 drosophila
37	30	62.5	584	1 LAM1_CHICK	P14731 gallus gall
38	30	62.5	585	1 LAM1_HUMAN	P20700 homo sapien
39	30	62.5	586	1 LAM1_RAT	P70615 rattus norv
40	30	62.5	587	1 LAM1_MOUSE	P14733 mus musculu
41	30	62.5	647	1 DPG1_CHICK	Q92076 gallus gall
42	30	62.5	878	1 MSH4_YEAST	P40965 saccharomyc
43	30	62.5	958	1 AMYG_DEBOC	P22861 debaryomyce
44	30	62.5	1018	1 DPOG_SCHPO	Q12704 schizosacch
45	30	62.5	1088	1 SEC8_SCHPO	O74562 schizosacch

ALIGNMENTS

RESULT 1
KV6A_MOUSE
ID KV6A_MOUSE STANDARD; PRT; 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; Pubmed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01941; KVMSX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
| | | | | | | | | |
Db 24 SASSSVSYMH 33

RESULT 2
KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 24.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11584 MW; 36E6D022A5EC34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 24 SASSSSVSYMH 33

RESULT 3
KV6C_MOUSE
ID KV6C_MOUSE STANDARD; PRT; 107 AA.
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 601).
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559(1978).
RN [2]
RP SEQUENCE (TEPC 191).
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites.";
RL proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -!- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
CC THAT BIND GALACTAN.
DR PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 24 SASSSSVSYMH 33

RESULT 4
KV6D_MOUSE
ID KV6D_MOUSE STANDARD; PRT; 107 AA.
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region SAPC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 24 SASSSSVSYMH 33

RESULT 5
KV6F_MOUSE

```
ID  KV6F_MOUSE  STANDARD; PRT; 107 AA.
AC  P04940;
DT  13-AUG-1987 (Rel. 05, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-VI region NQ2-17.4.1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83271467; PubMed=6877353;
RA  Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT  "mRNA sequences define an unusually restricted IgG response to 2-
RT  phenylloxazolone and its early diversification.";
RL  Nature 304:320-324(1983).
CC  -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; K00735; AAA38680.1; -.
DR  HSSP; P01679; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region; Hybridoma.
FT  DOMAIN 1 23 FRAMEWORK-1.
FT  DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 34 48 FRAMEWORK-2.
FT  DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 56 87 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-4.
FT  DOMAIN 97 106 FRAMEWORK-4.
FT  DISULFID 23 87 BY SIMILARITY.
FT  NON_TER 107 107
SQ  SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68E6 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 6
KV6G_MOUSE STANDARD; PRT; 107 AA.
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
```

```
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC -----
DR EMBL; K00737; AAA38682.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 7
KV6H_MOUSE STANDARD; PRT; 107 AA.
AC P04942;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ5-61.1.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC -----
DR EMBL; K00739; AAA38684.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
```

```
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;
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Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

```
RESULT 8
KV6I_MOUSE
ID KV6I_MOUSE STANDARD; PRT; 107 AA.
AC P04943;
```

DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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```
DR EMBL; K00740; AAA38685.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8E6 CRC64;
```

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

```
RESULT 9
KV6J_MOUSE
ID KV6J_MOUSE STANDARD; PRT; 107 AA.
AC P04944;
```

DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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DR EMBL; K00744; AAA38689.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Hybridoma.

```
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11611 MW; A38290781F3C30D3 CRC64;
```

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

```
RESULT 10
KV6K_MOUSE
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
```

DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -----
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CC -----
DR EMBL; K00746; AAA38691.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 99 108 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db 24 SASSSVSVMY 33
|||||||:

RESULT 11
KV6E_MOUSE
ID KV6E_MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; PubMed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01942; KVMSJ5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87
FT STRAND 4 7
FT STRAND 10 14
FT TURN 15 16
FT TURN 19 25
FT STRAND 31 37
FT STRAND 39 40
FT STRAND 44 48
FT TURN 49 51
FT STRAND 52 53
FT TURN 55 56
FT TURN 59 60
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 74
FT STRAND 79 81
FT HELIX 91 91
FT TURN 92 93
FT STRAND 94 97
FT STRAND 101 106
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;

Query Match 75.0%; Score 36; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db 24 SASSSVSSLH 33
|||||||:

RESULT 12
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -!- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
CC -----
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CC -----

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CC -----
DR EMBL; J00577; AAA38780.1; -.
DR EMBL; V00780; CAA24157.1; -.
DR PIR; A01943; KVM57B.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 58 72 FRAMEWORK-2.
FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 80 111 FRAMEWORK-3.
FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 128 FRAMEWORK-4.
FT DISULFID 45 111 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DCF6BE4 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 129;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 1;

QY 1 SASSSV--SYMH 10
   ||||| ||:|
Db 46 SASSSVSSSYLH 57

RESULT 13
ALYS_BPR1T STANDARD; PRT; 270 AA.
AC Q38135;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28).
OS Bacteriophage rlt.
OC Viruses.
OX NCBI_TaxID=43685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96332669; PubMed=8730875;
RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruitters M.H.,
RA Venema G., Nauta A.;
RT "Sequence analysis and molecular characterization of the temperate
RT lactococcal bacteriophage rlt.";
RL Mol. Microbiol. 19:1343-1355(1996).
CC -!- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl
CC residues and L-amino acid residues in certain bacterial cell-wall
CC glycopeptides.
CC -!- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
CC FAMILY 2.
CC -----
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CC -----
DR EMBL; U38906; AAB18724.1; -.
DR InterPro; IPR002502; Amidase_2.
DR Pfam; PF01510; Amidase_2; 1.
KW Hydrolase; Cell wall.
SQ SEQUENCE 270 AA; 30214 MW; 80A5E38F7F2A6675 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 270;
Best Local Similarity 60.0%; Pred. No. 7.7;
```

```
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
   ||:: ||||
Db 40 SATNEASVYM 49

RESULT 14
BGAL_MALDO STANDARD; PRT; 731 AA.
AC P48981;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-
DE galactosidase) (Exo-(1-->4)-beta-D-galactanase).
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv. Granny Smith; TISSUE=Fruit cortical tissue;
RX MEDLINE=95083752; PubMed=7991682;
RA Ross G.S., Wegrzyn T., Macrae E.A., Redgwell R.J.;
RT "Apple beta-galactosidase. Activity against cell wall polysaccharides
RT and characterization of a related cDNA clone.";
RL Plant Physiol. 106:521-528(1994).
CC -!- FUNCTION: Involved in cell wall degradation. Degrades
CC polysaccharides containing beta-(1-->4)-linked galactans, acting
CC as an exo-(1-->4)-beta-D-galactanase.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -!- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; L29451; AAA62324.1; -.
DR InterPro; IPR001944; GH_35.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
KW Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 731 BETA-GALACTOSIDASE.
FT ACT_SITE 182 182 PROTON DONOR (POTENTIAL).
FT ACT_SITE 251 251 NUCLEOPHILE (POTENTIAL).
SQ SEQUENCE 731 AA; 80995 MW; FAB65D24A0D30BD4 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 731;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
   :||:|||||
Db 21 AASASVSVDH 30

RESULT 15
RRF_SPIOL STANDARD; PRT; 271 AA.
AC P82231; Q9XG97;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome recycling factor, chloroplast precursor (Ribosome
```

DE releasing factor, chloroplast) (RRF) (CpFrr) (RRFHCP).
GN RRF OR FRRHCP.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 79-88.
RC TISSUE=Leaf;
RX MEDLINE=99254063; PubMed=10318906;
RA Rolland N., Janosi L., Block M.A., Shuda M., Teyssier E., Miege C.,
RA Cheniclet C., Carde J.-P., Kaji A., Joyard J.;
RT "Plant ribosome recycling factor homologue is a chloroplastic protein
RT and is bactericidal in Escherichia coli carrying temperature-sensitive
RT ribosome recycling factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:5464-5469(1999).
RN [2]
RP SEQUENCE OF 79-99 AND 194-217.
RC STRAIN=cv. Alvaro; TISSUE=Leaf;
RX PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: RESPONSIBLE FOR THE RELEASE OF RIBOSOMES FROM MESSENGER
CC RNA AT THE TERMINATION OF CHLOROPLASTIC PROTEIN BIOSYNTHESIS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST. THE MAJOR PART WAS FOUND IN THE
CC STROMA AND SOME PROTEIN WAS IN THE ENVELOPE SUBFRACTION, BUT NO
CC PROTEIN WAS DETECTED IN THE THYLAKOIDS.
CC -!- TISSUE SPECIFICITY: RESTRICTED TO PHOTOSYNTHETIC TISSUES.
CC -!- MISCELLANEOUS: EXPRESSION SEEMS TO BE LIGHT-INDEPENDANT.
CC -!- SIMILARITY: BELONGS TO THE RRF FAMILY.
CC -----
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CC -----
DR EMBL; AJ133751; CAB41419.1; -.
DR HSSP; Q9X1B9; 1DD5.
DR InterPro; IPR002661; RRF.
DR Pfam; PF01765; RRF; 1.
DR TIGRFAMs; TIGR00496; frr; 1.
KW Protein biosynthesis; Transit peptide; Chloroplast.
FT TRANSIT 1 78 CHLOROPLAST.
FT CHAIN 79 271 RIBOSOME RECYCLING FACTOR.
SQ SEQUENCE 271 AA; 30431 MW; F7D3012BB90AD175 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 271;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
I I I I I I I
Db 5 SLSSATSYLH 14

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 4.14729 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSVMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	97.9	134	11 Q8VDD0	Q8vdd0 mus musculu
2	44	91.7	97	11 Q9JL76	Q9jl76 mus musculu
3	43	89.6	235	11 Q91W12	Q91w12 mus musculu
4	38	79.2	106	5 Q9U410	Q9u410 schistosoma
5	37	77.1	547	2 Q59117	Q59117 arthrobacte
6	37	77.1	858	5 Q9V429	Q9v429 drosophila
7	36	75.0	991	5 Q9VIF5	Q9vif5 drosophila
8	35	72.9	200	3 Q08003	Q08003 saccharomyc
9	35	72.9	689	5 Q8T6L8	Q8t6l8 drosophila
10	35	72.9	720	3 Q14367	Q14367 schizosacch
11	35	72.9	1004	16 Q84646	Q84646 chlamydia t
12	35	72.9	1313	5 Q8T6L9	Q8t6l9 drosophila
13	34	70.8	537	16 Q98LI5	Q98li5 rhizobium l
14	34	70.8	731	10 Q9AYS1	Q9ays1 pyrus pyrif
15	34	70.8	1095	10 Q9C7S5	Q9c7s5 arabidopsis
16	34	70.8	1430	5 Q9W0B0	Q9w0b0 drosophila

17	34	70.8	1501	10 Q94LS3	Q94ls3 oryza sativ
18	34	70.8	2136	10 Q9SL97	Q9sl97 arabidopsis
19	33	68.8	101	11 Q9JL78	Q9jl78 mus musculu
20	33	68.8	234	3 Q94664	Q94664 schizosacch
21	33	68.8	347	8 Q9MM74	Q9mm74 acanthodact
22	33	68.8	382	2 Q9AMN1	Q9amn1 clostridium
23	33	68.8	463	11 Q99LC4	Q99lc4 mus musculu
24	33	68.8	477	16 Q97TF8	Q97tf8 clostridium
25	33	68.8	669	10 Q9SLC7	Q9slc7 arabidopsis
26	33	68.8	677	5 Q17720	Q17720 caenorhabdi
27	33	68.8	841	5 Q9VC32	Q9vc32 drosophila
28	33	68.8	944	5 Q18137	Q18137 caenorhabdi
29	33	68.8	1148	5 Q95ZY7	Q95zy7 caenorhabdi
30	33	68.8	1480	5 Q18138	Q18138 caenorhabdi
31	32	66.7	95	10 Q9M3C7	Q9m3c7 arabidopsis
32	32	66.7	158	10 Q9SIH6	Q9sih6 arabidopsis
33	32	66.7	206	5 Q9VK13	Q9vkl3 drosophila
34	32	66.7	219	16 Q9KBL2	Q9kbl2 bacillus ha
35	32	66.7	240	16 Q9KRV9	Q9krv9 vibrio chol
36	32	66.7	264	5 Q97455	Q97455 caenorhabdi
37	32	66.7	273	10 Q9SA31	Q9sa31 arabidopsis
38	32	66.7	288	5 Q19536	Q19536 caenorhabdi
39	32	66.7	294	1 Q74060	Q74060 cenarchaeum
40	32	66.7	303	4 Q9NSW1	Q9nsw1 homo sapien
41	32	66.7	363	16 Q9K9P1	Q9k9p1 bacillus ha
42	32	66.7	393	3 Q8X0D9	Q8x0d9 neurospora
43	32	66.7	411	4 Q13649	Q13649 homo sapien
44	32	66.7	451	16 Q9RK08	Q9rk08 streptomyce
45	32	66.7	510	16 Q9K3J1	Q9k3j1 streptomyce

ALIGNMENTS

RESULT 1

Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.

AC Q8VDD0;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Anti-MOG Z12 variable light chain (Fragment).

GN ANTI-MOG KAPPA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RA Chernajovsky Y.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RA Sembl P.;

RT *Targeting T cells to the CNS.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ416331; CAC94866.1; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IGv; 1.

FT NON_TER 134 134

SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 97.9%; Score 47; DB 11; Length 134;
Best Local Similarity 90.0%; Pred. No. 0.026;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 46 SASSTSYMH 55

RESULT 2

Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FF1F49DA1C CRC64;

Query Match 91.7%; Score 44; DB 11; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASSSVSYMH 10
Db 15 ASSSVSYMH 23

RESULT 3

Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 89.6%; Score 43; DB 11; Length 235;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSTSYMH 10

Db 46 SASSTSYMH 55

RESULT 4

Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 79.2%; Score 38; DB 5; Length 106;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSTSYMH 10
Db 24 SASSTSYMH 33

RESULT 5

Q59117 PRELIMINARY; PRT; 547 AA.
AC Q59117;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Choline oxidase (EC 1.1.3.17).
GN CODA.
OS Arthrobacter globiformis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococaceae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=1665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96145502; PubMed=8555454;
RA Deshniun P., Los D.A., Hayashi H., Mustardy L., Murata N.;
RT "Transformation of Synecoccus with a gene for choline oxidase
enhances tolerance to salt stress.";
RL Plant Mol. Biol. 29:897-907(1995).
DR EMBL; X84895; CAA59321.1; -.
DR HSSP; P22637; 3COX.
DR InterPro; IPR000172; GMC_oxred.
DR Pfam; PF00732; GMC_oxred; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
KW Oxidoreductase.
SQ SEQUENCE 547 AA; 58865 MW; 589175892034B3BE CRC64;

Query Match 77.1%; Score 37; DB 2; Length 547;
Best Local Similarity 77.8%; Pred. No. 16;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASSSVSYMH 10
:|||||:|

Db 208 SSSSVSYIH 216

RESULT 6
Q9V4Z9
ID Q9V4Z9 PRELIMINARY; PRT; 858 AA.
AC Q9V4Z9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CG11770 protein (LINES).
GN LIN OR CG11770.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20296724; PubMed=10837029;
RA Hatini V., Bokor P., Goto-Mandeville R., DiNardo S.;
RT "Tissue- and stage-specific modulation of Wingless signaling by the
RT segment polarity gene lines."
RL Genes Dev. 14:1364-1376(2000).
DR EMBL; AF003835; AAF59024.1; -.
DR EMBL; AF272358; AAF76228.1; -.
DR FlyBase; FBgn0002552; l1n.

SQ SEQUENCE 858 AA; 96291 MW; 95030ED5FE096139 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 858;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
:|||||

Db 366 STEASVSYMH 375

RESULT 7
Q9VIF5
ID Q9VIF5 PRELIMINARY; PRT; 991 AA.
AC Q9VIF5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG9252 protein.
GN CG9252.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003669; AAF53964.1; -.
DR FlyBase; FBgn0032920; CG9252.
SQ SEQUENCE 991 AA; 111757 MW; FFD72B5E86384155 CRC64;

Query Match 75.0%; Score 36; DB 5; Length 991;
Best Local Similarity 70.0%; Pred. No. 50;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
:|||:||||
Db 927 NASKSVSYMH 936

RESULT 8

Q08003
ID Q08003 PRELIMINARY; PRT; 200 AA.
AC Q08003;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chromosome XII reading frame ORF YLR073C.
GN YLR073C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Pohl T.M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; 273245; CAA97630.1; -.
DR SGD; S0004063; YLR073C.
SQ SEQUENCE; 200 AA; 22850 MW; 1C93378ED78C41A4 CRC64;

Query Match 72.9%; Score 35; DB 3; Length 200;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
:|||:||||
Db 75 SSSSSSYIH 84

RESULT 9

Q8T6L8
ID Q8T6L8 PRELIMINARY; PRT; 689 AA.
AC Q8T6L8;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Unconventional myosin 29D short isoform.
GN MYO29D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R; TISSUE=OVARY;
RA Tzolovskiy G., Bownes M., Millo H., Pathirana S., Wood T.;
RT "Identification and phylogenetic analysis of Drosophila melanogaster myosins";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AF454349; AAL91723.1; -.
SQ SEQUENCE 689 AA; 74009 MW; 9525A3C5B928FD2A CRC64;

Query Match 72.9%; Score 35; DB 5; Length 689;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
:|||:||||
Db 613 AASSAVSFLH 622

RESULT 10

O14367
ID O14367 PRELIMINARY; PRT; 720 AA.
AC O14367;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE GLUCONATE.
GN GTII.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP.011;
RX MEDLINE=98039718; PubMed=9372449;
RA Caspari T.;
RT "Onset of gluconate-H+ symport in Schizosaccharomyces pombe is regulated by the kinases Wis1 and Pkal, and requires the gtil+ gene product.";
RL J. Cell Sci. 110:2599-2608(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP.011;
RA Caspari T.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Zimmermann W., Wambutt R., McDougall R.C., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X92655; CAA63345.1; -.
DR EMBL; AL133154; CAB61447.1; -.
SQ SEQUENCE 720 AA; 78725 MW; 5CC2CD58ACE7CD87 CRC64;

Query Match 72.9%; Score 35; DB 3; Length 720;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASSSVSYMH 10
:||||:|:|
Db 255 SSSSLSYLH 263

RESULT 11

O84646
ID O84646 PRELIMINARY; PRT; 1004 AA.
AC O84646;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Exodeoxyribonuclease V, gamma.
GN RECC OR CT640.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis";
RL Science 282:754-759(1998).
DR EMBL; AE001334; AAC68244.1; -.
KW Complete proteome.
SQ SEQUENCE 1004 AA; 114401 MW; BB89266ED55F1496 CRC64;

Query Match 72.9%; Score 35; DB 16; Length 1004;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
I:|||||I
Db 108 SSSSEVSYSH 117

RESULT 12
Q8T6L9 Q8T6L9 PRELIMINARY; PRT; 1313 AA.
AC Q8T6L9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Unconventional myosin 29D.
GN MYO29D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R; TISSUE=OVARY;
RA Tzolovskiy G., Bownes M., Millo H., Pathirana S., Wood T.;
RT "Identification and phylogenetic analysis of Drosophila melanogaster
RT myosins.";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AF454348; AAL91722.1; -.
SQ SEQUENCE 1313 AA; 142708 MW; 1A164E5A073D9450 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 1313;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
I:|||||I
Db 1237 AASSAVSFLH 1246

RESULT 13
Q98LI5 Q98LI5 PRELIMINARY; PRT; 537 AA.
AC Q98LI5;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable dehydrogenase.
GN MLL1008.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002996; BAB48478.1; -.
DR InterPro; IPR000172; GMC_oxred.
DR Pfam; PF00732; GMC_oxred; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
KW Complete proteome.

SQ SEQUENCE 537 AA; 58507 MW; 250E2948450EC19D CRC64;

Query Match 70.8%; Score 34; DB 16; Length 537;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSSSVSYMH 10
I:|||||I
Db 192 SSAVSYLH 199

RESULT 14
Q9AYS1 Q9AYS1 PRELIMINARY; PRT; 731 AA.
AC Q9AYS1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23) (Lactase).
GN PJBGAL.
OS Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids I; Rosales; Rosaceae; Maloideae; Pyrus.
OX NCBI_TaxID=3767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HOUSUI; TISSUE=FRUIT;
RA Tateishi A., Inoue H., Shiba H., Yamaki S.;
RT "Molecular cloning of beta-galactosidase from Japanese pear (Pyrus
RT pyrifolia) and its gene expression with fruit ripening.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
CC -!- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.
DR EMBL; AB046543; BAB21492.1; -.
DR InterPro; IPR001944; GH_35.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 731 AA; 80922 MW; E069ACA689511514 CRC64;

Query Match 70.8%; Score 34; DB 10; Length 731;
Best Local Similarity 70.0%; Pred. No. 97;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
I:|||||I
Db 21 AASASVSYDH 30

RESULT 15
Q9C7S5 Q9C7S5 PRELIMINARY; PRT; 1095 AA.
AC Q9C7S5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Leucine-rich receptor-like protein kinase, putative, 84911-81624
DE (Putative leucine-rich receptor protein kinase).
GN T9N14.20 OR AT1G72300.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzialli A.,
RA Militschev J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yul G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequences and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana";
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC067754; AAG51803.1; -;
DR EMBL; AY080797; AAL87278.1; -;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 15.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00369; LRR_TYP; 6.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 1095 AA; 121520 MW; 52DECA8C2E0669BA CRC64;

Query Match 70.8%; Score 34; DB 10; Length 1095;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASSSVSYMH 10
|||::|||
Db 910 ASSGLAYMH 918

Search completed: December 23, 2002, 07:29:50
Job time : 7.14729 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 0.69186 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	28	90.3	204	1	YIP8_YEAST	P40451 saccharomyc
2	28	90.3	531	1	VL1_HPV16	P03101 human papil
3	28	90.3	601	1	YFK5_SCHPO	P87132 schizosacch
4	28	90.3	707	1	YJ9C_YEAST	P47166 saccharomyc
5	27	87.1	108	1	KV6K_MOUSE	P04945 mus musculu
6	27	87.1	126	1	YRP2_IRV6	P18306 chilo iride
7	27	87.1	129	1	KV4A_MOUSE	P01680 mus musculu
8	27	87.1	219	1	TR23_YEAST	Q03784 saccharomyc
9	27	87.1	255	1	YFCA_HAEIN	P46490 haemophilus
10	27	87.1	720	1	GTSE_HUMAN	Q9nyz3 homo sapien
11	27	87.1	919	1	YBO3_YEAST	P38073 saccharomyc
12	27	87.1	1477	1	KELC_DROME	Q04652 drosophila
13	26	83.9	87	1	IM08_YEAST	P57744 saccharomyc
14	26	83.9	173	1	SP12_YEAST	P17123 saccharomyc
15	26	83.9	334	1	E13B_HORVU	P15737 hordeum vul
16	26	83.9	348	1	YK51_YEAST	P36152 saccharomyc
17	26	83.9	352	1	NPII_ASPOR	P46076 aspergillus
18	26	83.9	382	1	YAE8_SCHPO	Q09848 schizosacch
19	26	83.9	469	1	VL2_BPVI	P03109 bovine papi
20	26	83.9	614	1	TU11_SCHPO	Q09715 schizosacch
21	26	83.9	687	1	YBG0_YEAST	P34225 saccharomyc
22	26	83.9	1050	1	ULK1_HUMAN	O75385 homo sapien
23	26	83.9	1398	1	MHP1_YEAST	P43638 saccharomyc
24	26	83.9	2504	1	FAS_HUMAN	P49327 homo sapien
25	26	83.9	2895	1	HYD_DROME	P51592 drosophila
26	25	80.6	209	1	V281_ARATH	Q9s9t7 arabidopsis
27	25	80.6	310	1	YC63_SYNY3	P74068 synechocyst
28	25	80.6	371	1	RLPA_ANASP	Q8ys24 anabaena sp
29	25	80.6	444	1	NU4M_LOCFI	Q36424 locusta mig
30	25	80.6	604	1	SP20_YEAST	P50875 saccharomyc
31	25	80.6	735	1	T2FA_YEAST	P41895 saccharomyc
32	25	80.6	838	1	FAS_MOUSE	P19096 mus musculu
33	25	80.6	932	1	HIRL_SCHPO	P87314 schizosacch

34	25	80.6	1060	1	YN18_YEAST	P53836 saccharomyc
35	25	80.6	1090	1	CYA2_RAT	P26769 rattus norv
36	25	80.6	1177	1	JAK_DROME	Q24592 drosophila
37	25	80.6	1275	1	YAU9_SCHPO	Q10164 schizosacch
38	25	80.6	1356	1	ROM2_YEAST	P51862 saccharomyc
39	25	80.6	1489	1	YGP0_YEAST	P53115 saccharomyc
40	25	80.6	1569	1	GLI3_XENLA	Q91660 xenopus lae
41	25	80.6	2505	1	FAS_RAT	P12785 rattus norv
42	24	77.4	103	1	YA40_MYCPN	P75074 mycoplasma
43	24	77.4	145	1	Y657_ARCFU	O29600 archaeoglob
44	24	77.4	154	1	YF12_MYCPN	P75274 mycoplasma
45	24	77.4	167	1	Y420_RICPR	Q9zdb2 rickettsia

ALIGNMENTS

```
RESULT 1
YIP8_YEAST
ID YIP8_YEAST STANDARD; PRT; 204 AA.
AC P40451;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 22.8 kDa protein in FOX3-UBP7 intergenic region.
GN YIL158W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YKR100C.
CC -----
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CC -----
CC EMBL; 238059; CAA86120.1; -.
DR PIR; S48376; S48376.
DR SGD; S0001420; YIL158W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 6 26 POTENTIAL.
SQ SEQUENCE 204 AA; 22840 MW; 7B86FA9F125F19BF CRC64;

Query Match 90.3%; Score 28; DB 1; Length 204;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||:|
Db 160 STSNLSS 166

RESULT 2
VL1_HPV16
ID VL1_HPV16 STANDARD; PRT; 531 AA.
AC P03101;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
```

DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=29900099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE OF 328-371 FROM N.A.
RX MEDLINE=92407963; PubMed=1326639;
RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
variants: a showcase for the molecular evolution of DNA viruses.";
RL J. Virol. 66:5714-5725(1992).
CC -I- MISCELLANEOUS: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE
CC OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.
CC
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CC
CC EMBL; K02718; AAA46943.1; -
DR EMBL; M96285; AAA47024.1; -
DR EMBL; A06331; CAA00546.1; -
DR PIR; A03640; P1WLHS.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_CAPSID_L1.
DR ProDom; PD000544; PV_capsid_L1; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 531 AA; 59554 MW; 5B3402587093B380 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 531;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 308 STANLAS 314

RESULT 3
YFK5_SCHPO STANDARD; PRT; 601 AA.
ID YFK5_SCHPO
AC P87132;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C167.05 in chromosome I.
GN SPAC167.05 OR SPAC57A7.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC
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CC
CC EMBL; AL035248; CAA22850.1; -
DR EMBL; Z95396; CAB08759.1; -
DR InterPro: IPR000041; Usp.
DR Pfam; PF00582; Usp; 1.
KW Hypothetical protein.
SQ SEQUENCE 601 AA; 65947 MW; 13FAACABDCE14239 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 601;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 143 STSNLAS 149

RESULT 4
YJ9C_YEAST STANDARD; PRT; 707 AA.
ID YJ9C_YEAST
AC P47166;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 81.2 kDa protein in NMD5-HOM6 intergenic region.
GN YJR134C OR J2120.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: SOME, TO PARAMYOSINS AND MYOSINS.
CC
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CC

```
DR EMBL; Z49634; CAA89665.1; -.
DR EMBL; Z49635; CAA89667.1; -.
DR SGD; S0003895; YJRI34C.
KW Hypothetical protein; Coiled coil.
FT DOMAIN 122 473 COILED COIL (POTENTIAL).
FT DOMAIN 594 706 COILED COIL (POTENTIAL).
SQ SEQUENCE 707 AA; 81171 MW; BA47DIA7265BF3D9 CRC64;

Query Match          90.3%; Score 28; DB 1; Length 707;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
   |||||:|
Db 25 STSNLSS 31

RESULT 5
KV6K_MOUSE
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -----
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CC -----
DR EMBL; K00746; AAA38691.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 99 108 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match          87.1%; Score 27; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNLAS 7
   |||||
Db 50 TSNLAS 55

RESULT 6
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```
YRP2_IRV6
ID YRP2_IRV6 STANDARD; PRT; 126 AA.
AC P18306;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Repetitive protein ORF2.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073753; PubMed=3201751;
RA Fischer M., Schnitzler P., Scholz J., Roesen-Wolff A., Delius H.,
RA Darai G.;
RT "DNA nucleotide sequence analysis of the PvUII DNA fragment L of the
RT genome of insect iridescent virus type 6 reveals a complex cluster of
RT multiple tandem, overlapping, and interdigitated repetitive DNA
RT elements.";
RL Virology 167:497-506(1988).
CC -!- SIMILARITY: A CONSENSUS SEQUENCE MANLX(6)IGSSSTX(6)LX(1)
CC LGSX(1)LQISGX(2)LX(1)VN WAS FOUND IN ALL FIVE ORFS.
CC -----
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CC -----
DR EMBL; M23625; AAA66587.1; -.
DR PIR; B31828; RPXFIJ.
KW Hypothetical protein.
FT SIMILAR 1 39 CONSERVED MOTIF IN THE FIVE ORFS.
SQ SEQUENCE 126 AA; 13371 MW; 2C927A1D41C41471 CRC64;

Query Match          87.1%; Score 27; DB 1; Length 126;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STSNLAS 7
   |||||
Db 15 STSNLVS 21

RESULT 7
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -!- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
CC -----
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DR EMBL; J00577; AAA38780.1; -.
DR EMBL; V00780; CAA24157.1; -.
DR PIR; A01943; KVM57B.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 58 72 FRAMEWORK-2.
FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 80 111 FRAMEWORK-3.
FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 128 FRAMEWORK-4.
FT DISULFID 45 111 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DCF6BE4 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNLAS 7
| | | | |
Db 74 TSNLAS 79

RESULT 8
TR23_YEAST
ID TR23_YEAST STANDARD; PRT; 219 AA.
AC Q03784;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transport protein particle 23 kDa subunit (TRAPP 23 kDa subunit).
GN TRS23 OR YDR246W OR YD8419.13.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]

RP IDENTIFICATION IN TRAPP COMPLEX.
RX MEDLINE=21664186; PubMed=11805826;
RA Gavin A.C., Bosche M., Krause M., Grandi P., Marzioch M., Bauer A.,
RA Schultze J., Rick J.M., Michon A.M., Cruciat C.M., Remor M., Hofert C.,
RA Schelder M., Brajenovic M., Ruffner H., Merino A., Klein K., Hudak M.,
RA Dickson D., Rudi T., Gnaul V., Bauch A., Bastuck S., Huhse B.,
RA Leutwein C., Heurtier M.A., Copley R.R., Edelmann A., Querfurth E.,
RA Rybin V., Drewes G., Raida M., Bouwmeester T., Bork P., Seraphin B.,
RA Kuster B., Neubauer G., Superti-Furga G.;
RT "Functional organization of the yeast proteome by systematic analysis
RT of protein complexes";
RL Nature 415:141-147(2002).
CC -!- FUNCTION: TRAPP plays a key role in the late stages of endoplasmic
CC reticulum to Golgi traffic.
CC -!- SUBUNIT: Part of multisubunit complex composed of BET3, BET5,
CC TRS20, TRS23, TRS31, TRS33, TRS65, TRS85, TRS120 and TRS130.
CC -!- SIMILARITY: BELONGS TO THE TRAPP SMALL SUBUNITS FAMILY.
CC TRS23 SUBFAMILY.

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DR EMBL; Z49701; CAA89732.1; -.
DR SGD; S0002654; TRS23.
KW Transport; Endoplasmic reticulum; Golgi stack.
SQ SEQUENCE 219 AA; 24863 MW; 8B32B1D5FE3846ED CRC64;

Query Match 87.1%; Score 27; DB 1; Length 219;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLA 6
| | | | |
Db 166 STSNLA 171

RESULT 9
YFCA_HAEIN STANDARD; PRT; 255 AA.
ID YFCA_HAEIN
AC P46490;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein HI0198.
GN HI0198.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]

RP REVISIONS.
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO E.COLI YFCA.
CC -!- SIMILARITY: TO M.LEPRAE U1177B.

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DR EMBL; U32705; AAC21867.1; -.
DR TIGR; HI0198; -.
DR InterPro; IPR002781; DUF81.
DR Pfam; PF01925; DUF81; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 7 27 POTENTIAL.


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FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 235 255 POTENTIAL.
SQ SEQUENCE 255 AA; 27608 MW; 7C0936C07F7B58F5 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNNLAS 7
Db 185 TSNNLAS 190

RESULT 10
GTSE_HUMAN STANDARD; PRT; 720 AA.
AC Q9NYZ3; Q9BRE0; Q9Y557; Q9UGZ9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE G2 and S phase expressed protein 1 (B99 homolog).
GN GTSE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20432105; PubMed=10974554;
RA Monte M., Collavin L., Lazarevic D., Utrera R., Dragani T.A.,
RA Schneider C.;
RT "Cloning, chromosome mapping and functional characterization of a
RT human homologue of murine Gtse-1 (B99) gene.";
RL Gene 254:229-236(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shlbuaya K., Yoshizaki Y., Aoki N., Mitsuama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
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RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in p53-induced cell cycle arrest in G2/M
CC phase by interfering with microtubule rearrangements that are
CC required to enter mitosis. Overexpression delays G2/M phase
CC progression.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.
CC -!- DEVELOPMENTAL STAGE: Expressed in G2/M phase. Not detected in
CC quiescent cells.
CC -!- PTM: Phosphorylated in mitosis (By similarity).
CC -----
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CC -----
DR EMBL; AF223408; AAF31459.1; -.
DR EMBL; AL031588; CAB38415.1; -.
DR EMBL; AL022325; CAB63079.1; -.
DR EMBL; BC006325; AAH06325.1; -.
KW Microtubules; Phosphorylation.
FT DOMAIN 22 27 POLY-SER.
FT CONFLICT 259 259 V -> I (IN REF. 1).
FT CONFLICT 506 506 R -> W (IN REF. 2; CAB38415).
SQ SEQUENCE 720 AA; 76614 MW; ACD91CCCD008A89C CRC64;

Query Match 87.1%; Score 27; DB 1; Length 720;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLA 6
Db 303 STSNLA 308
|||||

RESULT 11
YBO3_YEAST STANDARD; PRT; 919 AA.
AC P38073;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative 103.4 kDa transcriptional regulatory protein in RPL4A-HMT1
DE intergenic region.
GN YBR033W OR YBR0318.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=94378725; PubMed=8091864;
RA Smits P.H.M., de Haan M., Maat C., Grivell L.A.;
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RT "The complete sequence of a 33 kb fragment on the right arm of
RT chromosome II from Saccharomyces cerevisiae reveals 16 open reading
RT frames, including ten new open reading frames, five previously
RT identified genes and a homologue of the SCO1 gene.";
RL Yeast 10:575-S80(1994).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: CONTAINS 1 2N(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
CC CLUSTER DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X76078; CAA53688.1; -.
CC EMBL; Z35802; CAA84975.1; -.
CC PIR; S45889; S45889.
CC SGD; S0000237; YBR033W.
CC InterPro; IPR001138; Fungi_Trn.
CC Pfam; PF00172; Zn_clus; 1.
CC SMART; SM00066; GAL4; 1.
CC PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
CC PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
CC KW Hypothetical protein; Transcription regulation; DNA-binding;
CC KW Nuclear protein; Zinc; Metal-binding.
CC FT DNA_BIND 56 85 ZN(2)-CYS(6), FUNGAL-TYPE.
CC SEQUENCE 919 AA; 103396 MW; 18DD2E37A042E246 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 919;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TSNIAS 7
Db 756 TSNIAS 761
|||||

RESULT 12
KELC_DROME STANDARD; PRT; 1477 AA.
AC Q04652; Q04653; Q9VJA2;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ring canal kelch protein [Contains: Kelch short protein].
GN KEL OR CG7210.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93201592; PubMed=8453663;
RA Xue F., Cooley L.;
RT "Kelch encodes a component of intercellular bridges in Drosophila egg
RT chambers.";
RL Cell 72:681-693(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RN CHARACTERIZATION.
RP TISSUE=Embryo;
RX MEDLINE=97236487; PubMed=9118811;
RA Robinson D.N., Cooley L.;
RT "Examination of the function of two kelch proteins generated by stop
RT codon suppression.";
RL Development 124:1405-1417(1997).
CC -!- FUNCTION: COMPONENT OF RING CANALS THAT REGULATES THE FLOW OF
CC CYTOPLASM BETWEEN CELLS. MAY BE INVOLVED IN THE REGULATION OF
CC CYTOPLASM FLOW FROM NURSE CELLS TO THE OOCYTE DURING OOGENESIS.
CC BINDS ACTIN.
CC -!- SUBCELLULAR LOCATION: INNER SURFACE OF CYTOPLASMIC BRIDGES OR RING
CC CANALS PRESENT IN EGG CHAMBERS. SUBCORTICALLY IN IMAGINAL DISK
CC EPITHELIA.
CC -!- TISSUE SPECIFICITY: BOTH PROTEINS ARE EXPRESSED IN OVARIES, MALE
CC TESTIS, OVARECTOMIZED FEMALES, CUTICLE, SALIVARY GLAND AND
CC IMAGINAL DISKS. KELCH ORF1 IS THE PREDOMINANT PROTEIN AND IS ALSO
CC EXPRESSED IN FAT BODIES. ON ENTRY INTO METAMORPHOSIS LEVELS OF
CC FULL LENGTH PROTEIN INCREASE IN TESTIS AND IMAGINAL DISKS.
CC -!- DEVELOPMENTAL STAGE: LARVAE, PUPAE AND ADULTS.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC -!- CAUTION: REF.3 BELIEVES RESIDUE 690 IS A SELENOCYSTEINE.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
CC EMBL; L08483; AAA53471.1; -.
CC EMBL; L08483; AAA53472.2; -.
CC EMBL; AE003657; AAF53651.1; ALT_SEQ.
CC HSSP; Q05516; 1CS3.
CC FlyBase; FBgn0001301; kel.
CC InterPro; IPR000210; BTB_POZ.
CC InterPro; IPR001798; Kelch.
```

DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
KW Cytoskeleton; Actin-binding; Selenium; Selenocysteine; Repeat.
FT CHAIN 1 1477
FT CHAIN 1 689
FT DOMAIN 157 223
FT REPEAT 404 449
FT REPEAT 450 496
FT REPEAT 498 543
FT REPEAT 545 592
FT REPEAT 594 639
FT REPEAT 641 687
FT DOMAIN 18 28
FT DOMAIN 29 87
FT DOMAIN 29 36
FT DOMAIN 78 83
FT SE_CYS 690 690
FT CONFLICT 493 493
FT CONFLICT 596 596
FT CONFLICT 824 824
FT CONFLICT 858 858
FT CONFLICT 1083 1083
FT CONFLICT 1086 1086
SQ SEQUENCE 1477 AA; 160086 MW; 4851EEAE9D9DBA47 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 1477;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNNLAS 7
Db 650 TSNNLAS 655

RESULT 13
IM08_YEAST
ID IM08_YEAST STANDARD; PRT; 87 AA.
AC P57744;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM8.
GN TIM8 OR YJRL35W-A OR YJRL35BW.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC
CC
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CC
CC EMBL; Z49636; -; NOT_ANNOTATED_CDS.
DR SGD; S0007348; TIM8.
DR InterPro; IPR004217; Znf_Tim10/DDP.
DR Pfam; PF02953; zf-Tim10-DDP; 1.
KW Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
SQ SEQUENCE 87 AA; 9764 MW; B91D1DD41707EA24 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 87;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 5 STSNLAS 11

RESULT 14
SP12_YEAST
ID SP12_YEAST STANDARD; PRT; 173 AA.
AC P17123;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sporulation protein SPO12.
GN SPO12 OR YHR152W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90258869; PubMed=2188099;
RA Malavasic M.J., Elder R.T.;
RT "Complementary transcripts from two genes necessary for normal
RT meiosis in the yeast Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 10:2809-2819(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
CC -!- FUNCTION: IT IS REQUIRED FOR MEIOSIS I CHROMOSOME DIVISION DURING
CC SPORULATION.
CC -!- MISCELLANEOUS: ITS NEGATIVE TAIL IS FUNCTIONALLY IMPORTANT.
CC -!- SIMILARITY: TO YEAST G8558.
CC
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CC
CC EMBL; M32653; AAA35076.1; -;
DR EMBL; U10397; AAB68979.1; -;
DR PIR; B36321; B36321.
DR PIR; S46756; S46756.
DR SGD; S0001195; SPO12.
KW Sporulation; Meiosis.
FT DOMAIN 159 173
SQ SEQUENCE 173 AA; 19912 MW; E114394516451F60 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 173;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 78 STSNLAS 84

RESULT 15
E13B_HORVU
ID E13B_HORVU STANDARD; PRT; 334 AA.
AC P15737;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucan endo-1,3-beta-glucosidase GII precursor (EC 3.2.1.39) ((1->3)-
DE beta-glucan endohydrolase GII) ((1->3)-beta-glucanase isoenzyme GII)
DE (Beta-1,3-endoglucanase GII).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-68.
RC STRAIN=cv. Clipper;
RX MEDLINE=93357431; PubMed=2562758;
RA Hoej P.B., Hartman D.J., Morrice N.A., Doan D.N.P., Fincher G.B.;
RT "Purification of (1->3)-beta-glucan endohydrolase isoenzyme II from
RT germinated barley and determination of its primary structure from a
RT cDNA clone.";
RL Plant Mol. Biol. 13:31-42(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Piggy;
RX MEDLINE=91107649; PubMed=1899089;
RA Leah R., Tommerup H., Svendsen I., Mundy J.;
RT "Biochemical and molecular characterization of three barley seed
RT proteins with antifungal properties.";
RL J. Biol. Chem. 266:1564-1573(1991).
RN [3]
RP SEQUENCE OF 258-332 FROM N.A.
RC TISSUE=Leaf;
RA Jutidamrongphan W., Mackinnon G., Manners J., Simpson R.S.,
RA Scott K.J.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 29-334.
RA Ballance G.M., Svendsen I.;
RT "Purification and amino acid sequence determination of an endo-1,3-
RT beta-glucanase from barley.";
RL Carlsberg Res. Commun. 53:411-419(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=94195828; PubMed=8146192;
RA Varghese J.N., Garrett T.P.J., Colman P.M., Chen L., Hoej P.B.,
RA Fincher G.B.;
RT "Three-dimensional structures of two plant beta-glucan endohydrolases
RT with distinct substrate specificities.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2785-2789(1994).
CC -!- FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL
CC INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE
CC FUNGAL CELL WALL POLYSACCHARIDES.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC -!- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL; M62907; AAA32939.1; -
DR EMBL; X16274; CAA34350.1; -
DR EMBL; M23548; AAA32958.1; -
DR PIR; S05510; S05510.
DR PIR; A31800; A31800.

PDB; 1GHS; 01-NOV-94.
DR InterPro; IPR000490; Glyco_hydro_17.
DR Pfam; PF00332; Glyco_hydro_17; 1.
DR PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
KW Hydrolase; Glycosidase; Signal; Multigene family; 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 334 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GII.
FT ACT_SITE 259 259 NUCLEOPHILE.
FT ACT_SITE 316 316 PROTON DONOR.
FT CONFLICT 12 12 A -> V (IN REF. 2).
FT CONFLICT 71 71 L -> V (IN REF. 2).
SQ SEQUENCE 334 AA; 35193 MW; 552D66A29A08C703 CRC64;
Query Match 83.9%; Score 26; DB 1; Length 334;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 93 STSNAAS 99

Search completed: December 23, 2002, 07:26:08
Job time : 2.69186 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 2.9031 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	31	100.0	265	16	Q8YDZ0	Q8ydz0 brucella me
2	31	100.0	388	2	Q9KIS6	Q9kis6 brucella ab
3	31	100.0	391	2	Q9RPX5	Q9rpx5 brucella su
4	31	100.0	595	9	Q37901	Q37901 bacterioph
5	31	100.0	753	5	Q26306	Q26306 drosophila
6	31	100.0	1107	3	Q12271	Q12271 saccharomyc
7	28	90.3	97	11	Q9JL76	Q9jl76 mus musculu
8	28	90.3	187	10	Q9C5K8	Q9c5k8 arabidopsis
9	28	90.3	401	3	Q8X084	Q8x084 neurospora
10	28	90.3	494	12	Q80996	Q80996 human papil
11	28	90.3	494	12	Q80997	Q80997 human papil
12	28	90.3	494	12	Q80998	Q80998 human papil
13	28	90.3	494	12	Q80999	Q80999 human papil
14	28	90.3	494	12	Q81000	Q81000 human papil
15	28	90.3	494	12	Q81001	Q81001 human papil
16	28	90.3	494	12	Q81002	Q81002 human papil

17	28	90.3	494	12	Q81004	Q81004 human papil
18	28	90.3	494	12	Q81005	Q81005 human papil
19	28	90.3	494	12	Q81006	Q81006 human papil
20	28	90.3	494	12	Q81007	Q81007 human papil
21	28	90.3	494	12	Q81008	Q81008 human papil
22	28	90.3	494	12	Q81009	Q81009 human papil
23	28	90.3	494	12	Q81010	Q81010 human papil
24	28	90.3	494	12	Q81011	Q81011 human papil
25	28	90.3	494	12	Q81012	Q81012 human papil
26	28	90.3	494	12	Q90204	Q90204 human papil
27	28	90.3	495	12	Q12343	Q12343 human papil
28	28	90.3	505	12	Q9WLQ5	Q9wlq5 human papil
29	28	90.3	505	12	Q92282	Q92282 human papil
30	28	90.3	505	12	Q9WHS5	Q9whs5 human papil
31	28	90.3	505	12	Q9WHS6	Q9whs6 human papil
32	28	90.3	505	12	Q9WPH4	Q9wph4 human papil
33	28	90.3	505	12	Q9WLQ6	Q9wlq6 human papil
34	28	90.3	522	3	Q96VF4	Q96vf4 uromyces fa
35	28	90.3	531	12	O00530	O00530 human papil
36	28	90.3	531	16	Q8Z0P3	Q8z0p3 anabaena sp
37	28	90.3	567	3	P78871	P78871 schizosacch
38	28	90.3	597	16	Q9PPX0	Q9ppx0 ureaplasma
39	28	90.3	963	16	O07232	O07232 mycobacteri
40	28	90.3	1026	5	Q961S4	Q961s4 drosophila
41	28	90.3	1333	5	Q24262	Q24262 drosophila
42	28	90.3	3186	16	Q8VKN2	Q8vkn2 mycobacteri
43	27	87.1	101	11	Q9JL78	Q9jl78 mus musculu
44	27	87.1	106	5	Q9U410	Q9u410 schistosoma
45	27	87.1	135	5	Q95Z75	Q95z75 ostertagia

ALIGNMENTS

RESULT 1

Q8YDZ0 ID Q8YDZ0 PRELIMINARY; PRT; 265 AA.
AC Q8YDZ0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Channel protein VIRB10 homolog.
GN BMEI10034.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009642; AAL53275.1; -.
KW Complete proteome.
SQ SEQUENCE 265 AA; 28204 MW; 042033AA2FD5EC73 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 219 STSNLAS 225

RESULT 2

Q9KIS6
ID Q9KIS6 PRELIMINARY; PRT; 388 AA.
AC Q9KIS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VirB10.
GN VIRB10.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RX MEDLINE=20398168; PubMed=10940027;
RA Sleira R.; Comerici D.J.; Sanchez D.O.; Ugalde R.A.;
RT "A Homologue of an Operon Required for DNA Transfer in Agrobacterium
RT Is Required in Brucella abortus for Virulence and Intracellular
RT Multiplication.";
RL J. Bacteriol. 182:4849-4855(2000).
DR EMBL; AF226278; AAF73903.1; -.
SQ SEQUENCE 388 AA; 41193 MW; D8A63372B267E7F3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 388;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 342 STSNLAS 348

RESULT 3
Q9RPX5
ID Q9RPX5 PRELIMINARY; PRT; 391 AA.
AC Q9RPX5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VirB10.
GN VIRB10.
OS Brucella suis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330;
RX MEDLINE=99440171; PubMed=10510235;
RA O'Callaghan D.; Cazevielle C.; Allardet-Servent A.; Boschirolli M.L.;
RA Bourg G.; Foulongne V.; Frutos P.; Kulakov Y.; Ramuz M.;
RT "A homologue of the Agrobacterium tumefaciens VirB and Bordetella
RT pertussis Ptl type IV secretion systems is essential for intracellular
RT survival of Brucella suis.";
RL Mol. Microbiol. 33:1210-1220(1999).
DR EMBL; AF141604; AAD56620.1; -.
SQ SEQUENCE 391 AA; 41453 MW; A6DCA4C9AFBB490D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 345 STSNLAS 351

RESULT 4
Q37901
ID Q37901 PRELIMINARY; PRT; 595 AA.
AC Q37901;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tail protein.
GN HRS.
OS Bacteriophage BF23.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC T5-like viruses.
OX NCBI_TaxID=10707;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96204568; PubMed=86233528;
RA Mondigler M.; Holz T.; Heller K.J.;
RT "Identification of the receptor-binding regions of pb5 proteins of
RT bacteriophages T5 and BF23.";
RL Virology 219:19-28(1996).
DR EMBL; L42820; AAB05216.1; -.
SQ SEQUENCE 595 AA; 63909 MW; E79B717F88EA2099 CRC64;

Query Match 100.0%; Score 31; DB 9; Length 595;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 264 STSNLAS 270

RESULT 5
Q26306
ID Q26306 PRELIMINARY; PRT; 753 AA.
AC Q26306;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEU=NEURALIZED.
GN NEUR OR NEU OR CG11988.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93285130; PubMed=8508781;
RA Boulianne G.L.; la Concha A.; Campos-Ortega J.A.; Jan L.Y.; Jan Y.N.;
RT "The Drosophila neurogenic gene neuralized encodes a novel protein and
RT is expressed in precursors of larval and adult neurons.";
RL EMBO J. 12:2586-2586(1993).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; S62597; AAB27151.1; -.
DR FlyBase; FBgn0002932; neur.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 753 AA; 82307 MW; 45056A93EDDA7B41 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 585 STSNLAS 591

RESULT 6
Q12271
ID Q12271 PRELIMINARY; PRT; 1107 AA.
AC Q12271;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE YOR3231W from chromosome XV.
GN INP53 OR YOR3231W OR YOR109W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Andrade M.A., Rechmann S., Teodoru C., Banrevi A.,
RA Sander C., Valencia A., Ansorge W., Voss H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Voss H., Benes V., Rechmann S., Teodoru C., Schwager C., Paces V.,
RA Ansorge W.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94335; CAA64029.1; -;
DR EMBL; Z75017; CAA99307.1; -;
DR SGD; S0005635; INP53.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000300; IPPC.
DR InterPro; IPR002013; Syja_N.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF02383; Syja_N; 1.
DR SMART; SM00128; IPPC; 1.
SQ SEQUENCE 1107 AA; 124576 MW; 1E024F15085261EA CRC64;

Query Match 100.0%; Score 31; DB 3; Length 1107;
Best Local Similarity 100.0%; Pred. NO. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 1029 STSNLAS 1035
|||||

RESULT 7
Q9JL76
ID Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -;
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 1
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;

Query Match 90.3%; Score 28; DB 11; Length 97;

Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 39 ATSNLAS 45
:|||||

RESULT 8
Q9C5K8
ID Q9C5K8 PRELIMINARY; PRT; 187 AA.
AC Q9C5K8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 19.9 kDa protein.
GN F22D1.70/AT5G20900.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene F22D1.70/AT5g20900.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene F22D1.70/AT5g20900.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360184; AAK25894.1; -;
DR EMBL; AY051013; AAK93690.1; -;
DR InterPro; IPR000194; ATPase_alpha_betacentre.
DR PROSITE; PS00152; ATPase_ALPHA_BETA; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 19933 MW; 4F0C66DECB4F0E1 CRC64;

Query Match 90.3%; Score 28; DB 10; Length 187;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 112 STSNVAS 118
|||||

RESULT 9
Q8X084
ID Q8X084 PRELIMINARY; PRT; 401 AA.
AC Q8X084;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Related to vegetative cell wall protein gpl.
GN B14D6.440.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.

```
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL356173; CAB91753.2; -
SQ SEQUENCE: 401 AA; 42038 MW; 0933A161C07B92EA CRC64;

Query Match 90.3%; Score 28; DB 3; Length 401;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 358 STSNLAS 364

RESULT 10
Q80996
ID Q80996 PRELIMINARY; PRT; 494 AA.
AC Q80996;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM 4094;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NM 4094;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NM 4094;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34165; AAA91712.1; -
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55063 MW; 735F7C2B86CAC58F CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 273 STSNLAS 279

RESULT 11
Q80997
ID Q80997 PRELIMINARY; PRT; 494 AA.
AC Q80997;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
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DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM 9999;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NM 9999;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34166; AAA91713.1; -
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55063 MW; 735F7C2B86CAC58F CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 273 STSNLAS 279

RESULT 12
Q80998
ID Q80998 PRELIMINARY; PRT; 494 AA.
AC Q80998;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM T197;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NM T197;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NM T197;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34167; AAA91714.1; -
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
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DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55021 MW; E446FD38994FB3DD CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 273 STANLAS 279

RESULT 13
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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM T455;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
||:||||
Db 273 STANLAS 279

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
||:||||
Db 273 STANLAS 279

RESULT 14
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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM T529;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NM T529;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34170; AAA91717.1; -
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55063 MW; 735F7C2B86CAC58F CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 273 STANLAS 279

RESULT 15
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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR 1905;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OR 1905;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34172; AAA91719.1; -
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55094 MW; ECB31B09E8EFB4E3 CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OR 1905;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34172; AAA91719.1; -
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55094 MW; ECB31B09E8EFB4E3 CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
||:||||
Db 273 STANLAS 279

Search completed: December 23, 2002, 07:29:52
Job time : 4.9031 secs

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OM protein - protein search, using sw model

Run on: Decembar 23, 2002, 07:20:23 ; Search time 1.62209 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QORSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	93.8	9	2	US-08-116-778E-11 Sequence 11, Appl
2	45	93.8	9	2	US-08-438-562-11 Sequence 11, Appl
3	45	93.8	9	2	US-08-483-528B-99 Sequence 99, Appl
4	45	93.8	9	4	US-09-393-385B-110 Sequence 110, App
5	45	93.8	129	2	US-08-116-778E-2 Sequence 2, Appli
6	45	93.8	129	2	US-08-438-562-2 Sequence 2, Appli
7	45	93.8	129	2	US-08-483-528B-92 Sequence 92, Appl
8	45	93.8	130	4	US-09-393-385B-111 Sequence 111, App
9	45	93.8	130	4	US-09-393-385B-113 Sequence 113, App
10	45	93.8	133	2	US-08-116-778E-37 Sequence 37, Appl
11	45	93.8	133	2	US-08-438-562-37 Sequence 37, Appl
12	45	93.8	133	2	US-08-483-528B-101 Sequence 101, App
13	42	87.5	270	2	US-08-652-507-2 Sequence 2, Appli
14	42	87.5	553	2	US-08-661-052-16 Sequence 16, Appl
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16	42	87.5	553	4	US-09-364-088-16 Sequence 16, Appl
17	42	87.5	553	4	US-09-102-716-16 Sequence 16, Appl
18	39	81.2	9	4	US-09-171-945-28 Sequence 28, Appl
19	39	81.2	107	4	US-09-171-945-50 Sequence 50, Appl
20	39	81.2	107	4	US-09-171-945-61 Sequence 61, Appl
21	39	81.2	107	4	US-09-171-945-65 Sequence 65, Appl
22	39	81.2	107	4	US-09-171-945-71 Sequence 71, Appl
23	39	81.2	108	4	US-09-171-945-9 Sequence 9, Appli
24	39	81.2	235	4	US-09-171-945-17 Sequence 17, Appl
25	39	81.2	235	4	US-09-171-945-52 Sequence 52, Appl
26	39	81.2	235	4	US-09-171-945-97 Sequence 97, Appl
27	39	81.2	235	4	US-09-171-945-99 Sequence 99, Appl

28	39	81.2	281	4	US-09-423-439-44	Sequence 44, Appl
29	39	81.2	666	4	US-09-423-439-51	Sequence 51, Appl
30	38	79.2	108	2	US-08-378-939-32	Sequence 32, Appl
31	38	79.2	108	2	US-08-378-939-34	Sequence 34, Appl
32	37	77.1	105	3	US-08-434-000A-12	Sequence 12, Appl
33	37	77.1	105	4	US-09-312-157-12	Sequence 12, Appl
34	37	77.1	230	4	US-09-485-737B-102	Sequence 102, App
35	37	77.1	233	4	US-09-485-737B-69	Sequence 69, Appl
36	37	77.1	235	4	US-09-485-737B-93	Sequence 93, Appl
37	37	77.1	240	4	US-09-485-737B-91	Sequence 91, Appl
38	37	77.1	267	4	US-09-485-737B-2	Sequence 2, Appli
39	37	77.1	541	4	US-09-485-737B-85	Sequence 85, Appl
40	37	77.1	711	4	US-09-485-737B-90	Sequence 90, Appl
41	36	75.0	108	4	US-09-157-370-4	Sequence 4, Appli
42	36	75.0	130	2	US-08-659-567-2	Sequence 2, Appli
43	36	75.0	249	2	US-08-797-689-18	Sequence 18, Appl
44	35	72.9	107	3	US-08-554-840-1	Sequence 1, Appli
45	35	72.9	107	3	US-08-554-840-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-116-778E-11
; Sequence 11, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-116-778E-11

Query Match 93.8%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QORSSYPFT 9
|||||||:|

Db 1 QORSSYPYT 9

RESULT 2

US-08-438-562-11
; Sequence 11, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-438-562-11

Query Match 93.8%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPYT 9

Db 1 QORSSYPYT 9

RESULT 3

US-08-483-528B-99
; Sequence 99, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,528B

FILING DATE: 07-JUN-95

CLASSIFICATION: 536

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-483-528B-99

Query Match 93.8%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPYT 9

Db 1 QORSSYPYT 9

RESULT 4

US-09-393-385B-110
; Sequence 110, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI

APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO

APPLICANT: KUWANA, YOSHIHISA

APPLICANT: HASEGAWA, MAMORU

TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/393,385B

FILING DATE: 27-JUN-96

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 110:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-393-385B-110

Query Match 93.8%; Score 45; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | | | |
Db 1 QQRSSYPFT 9

RESULT 5

US-08-116-778E-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22...-1
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; IDENTIFICATION METHOD: /product= "HYPERVARIABLE REGION 1"

; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED

; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-116-778E-2

Query Match 93.8%; Score 45; DB 2; Length 129;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | | | |
Db 110 QQRSSYPFT 118

RESULT 6

US-08-438-562-2
; Sequence 2, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22...-1
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; FEATURE:

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; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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US-08-438-562-2
Query Match 93.8%; Score 45; DB 2; Length 129;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
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Db 110 QORSSYPYT 118

RESULT 7
US-08-483-528B-92
; Sequence 92; Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELEPHONE: (703)816-4100
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD:

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; IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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US-08-483-528B-92
Query Match 93.8%; Score 45; DB 2; Length 129;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
   |||||:|
Db 110 QORSSYPYT 118

RESULT 8
US-09-393-385B-111
; Sequence 111; Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-393-385B-I11

Query Match 93.8%; Score 45; DB 4; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
Db 110 QORSSYPYT 118

RESULT 9

US-09-393-385B-113
; Sequence 113, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:

; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-393-385B-113

Query Match 93.8%; Score 45; DB 4; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
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Db 110 QORSSYPYT 118

RESULT 10

US-08-116-778E-37
; Sequence 37, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES

; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-778E-37

Query Match 93.8%; Score 45; DB 2; Length 133;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
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Db 110 QORSSYPYT 118

RESULT 11

US-08-438-562-37
; Sequence 37, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-562-37

Query Match 93.8%; Score 45; DB 2; Length 133;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSSYPFT 9
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Db 110 QQRSSYPYT 118

RESULT 12
US-08-483-528B-101
Sequence 101, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-528B-101

Query Match 93.8%; Score 45; DB 2; Length 133;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSSYPFT 9
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Db 110 QQRSSYPYT 118

RESULT 13
US-08-652-507-2
Sequence 2, Application US/08652507
Patent No. 5876691
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5876691th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-2

Query Match 87.5%; Score 42; DB 2; Length 270;
Best Local Similarity 88.9%; Pred. No. 0.92;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSSYPFT 9
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Db 249 QQRSSYPYT 257

RESULT 14
US-08-661-052-16
Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-661-052-16

Query Match 87.5%; Score 42; DB 2; Length 553;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
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Db 499 QQRSSYPFT 507

RESULT 15

US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-09-188-082-16
Query Match 87.5%; Score 42; DB 4; Length 553;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
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Db 499 QQRSSYPFT 507

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OM protein - protein search, using sw model

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(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	48	100.0	106	10	US-09-976-787-24	Sequence 24, Appl
4	48	100.0	106	10	US-09-865-198-23	Sequence 23, Appl
5	48	100.0	108	10	US-09-976-787-8	Sequence 8, Appli
6	48	100.0	108	10	US-09-865-198-8	Sequence 8, Appli
7	48	100.0	131	10	US-09-881-823-6	Sequence 6, Appli
8	48	100.0	238	10	US-09-976-787-29	Sequence 29, Appl
9	48	100.0	238	10	US-09-865-198-28	Sequence 28, Appl
10	48	100.0	240	10	US-09-976-787-28	Sequence 28, Appl
11	48	100.0	240	10	US-09-865-198-27	Sequence 27, Appl
12	45	93.8	107	9	US-09-144-886-88	Sequence 88, Appl
13	45	93.8	112	9	US-09-144-886-89	Sequence 89, Appl
14	43	89.6	9	10	US-09-808-037-17	Sequence 17, Appl
15	43	89.6	9	10	US-09-808-037-19	Sequence 19, Appl
16	43	89.6	119	10	US-09-808-037-28	Sequence 28, Appl
17	43	89.6	239	10	US-09-808-037-6	Sequence 6, Appli
18	40	83.3	9	10	US-09-808-037-18	Sequence 18, Appl
19	40	83.3	107	9	US-09-144-886-75	Sequence 75, Appl

20	39	81.2	9	10	US-09-910-059-28	Sequence 28, Appl
21	39	81.2	107	10	US-09-910-059-50	Sequence 50, Appl
22	39	81.2	107	10	US-09-910-059-61	Sequence 61, Appl
23	39	81.2	107	10	US-09-910-059-65	Sequence 65, Appl
24	39	81.2	107	10	US-09-910-059-71	Sequence 71, Appl
25	39	81.2	108	10	US-09-910-059-9	Sequence 9, Appli
26	39	81.2	235	10	US-09-910-059-17	Sequence 17, Appl
27	39	81.2	235	10	US-09-910-059-52	Sequence 52, Appl
28	39	81.2	235	10	US-09-910-059-97	Sequence 97, Appl
29	39	81.2	235	10	US-09-910-059-99	Sequence 99, Appl
30	37	77.1	105	9	US-09-982-107-12	Sequence 12, Appl
31	37	77.1	669	9	US-09-807-721-2	Sequence 2, Appli
32	36	75.0	249	10	US-09-984-186-18	Sequence 18, Appl
33	35	72.9	9	10	US-09-808-037-15	Sequence 15, Appl
34	35	72.9	9	10	US-09-808-037-16	Sequence 16, Appl
35	35	72.9	9	10	US-09-808-037-20	Sequence 20, Appl
36	34	70.8	107	9	US-09-144-886-78	Sequence 78, Appl
37	34	70.8	109	9	US-09-144-886-79	Sequence 79, Appl
38	34	70.8	109	9	US-09-144-886-96	Sequence 96, Appl
39	33	68.8	53	10	US-09-867-550-1076	Sequence 1076, Ap
40	32	66.7	9	9	US-09-771-415-5	Sequence 5, Appli
41	32	66.7	9	9	US-09-996-288-6	Sequence 6, Appli
42	32	66.7	9	10	US-09-796-848A-7	Sequence 7, Appli
43	32	66.7	9	10	US-09-828-708-51	Sequence 51, Appl
44	32	66.7	102	10	US-09-905-243-80	Sequence 80, Appl
45	32	66.7	104	10	US-09-828-708-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-976-787-6
; Sequence 6, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-6

Query Match 100.0%; Score 48; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | | | |
Db 1 QQRSSYPFT 9

RESULT 2
US-09-865-198-6
; Sequence 6, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-6

Query Match 100.0%; Score 48; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
Db 1 QORSSYPFT 9

RESULT 3

US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
Db 88 QORSSYPFT 96

RESULT 4

US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
Db 88 QORSSYPFT 96

RESULT 5

US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
Db 88 QORSSYPFT 96

RESULT 6

US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
Db 88 QORSSYPFT 96

RESULT 7

US-09-881-823-6

; Sequence 6, Application US/09881823
; Patent No. US2002006806A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-6

Query Match 100.0%; Score 48; DB 10; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
|||||
Db 110 QORSSYPFT 118

RESULT 8

US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
|||||
Db 220 QORSSYPFT 228

RESULT 9

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102

; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
|||||
Db 220 QORSSYPFT 228

RESULT 10

US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
|||||
Db 220 QORSSYPFT 228

RESULT 11

US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
|||||

Db 220 QQRSSYPFT 228

RESULT 12

US-09-144-886-88
; Sequence 88; Application US/09144886
; Patent No. US20020155114A1

GENERAL INFORMATION:

APPLICANT: Marks, James D

APPLICANT: Amersdorfer, Peter

TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize

TITLE OF INVENTION: Botulinum Neurotoxins

FILE REFERENCE: 2500.117USO

CURRENT APPLICATION NUMBER: US/09/144,886

CURRENT FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 88

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: BONT/a clone

OTHER INFORMATION: 2G5 region VL epitope 2

US-09-144-886-88

Query Match 93.8%; Score 45; DB 9; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
|||||

Db 88 QQRSSYPFT 96

RESULT 13

US-09-144-886-88
; Sequence 89; Application US/09144886
; Patent No. US20020155114A1

GENERAL INFORMATION:

APPLICANT: Marks, James D

APPLICANT: Amersdorfer, Peter

TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize

TITLE OF INVENTION: Botulinum Neurotoxins

FILE REFERENCE: 2500.117USO

CURRENT APPLICATION NUMBER: US/09/144,886

CURRENT FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 89

LENGTH: 112

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone

OTHER INFORMATION: 3C3 region VL epitope 2

US-09-144-886-89

Query Match 93.8%; Score 45; DB 9; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
|||||

Db 93 QQRSSYPFT 101

RESULT 14
US-09-808-037-17
; Sequence 17; Application US/09808037
; Patent No. US20020052311A1

GENERAL INFORMATION:

APPLICANT: SOLOMON, Beka

APPLICANT: HANAN, Eilat

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

FILE REFERENCE: SOLOMON-2D

CURRENT APPLICATION NUMBER: US/09/808,037

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/629,971

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/473,653

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: US 60/152,417

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.0

SEQ ID NO 17

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic peptide

US-09-808-037-17

Query Match 89.6%; Score 43; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
|||||

Db 2 QRSSYPFT 9

RESULT 15

US-09-808-037-19
; Sequence 19; Application US/09808037
; Patent No. US20020052311A1

GENERAL INFORMATION:

APPLICANT: SOLOMON, Beka

APPLICANT: HANAN, Eilat

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

FILE REFERENCE: SOLOMON-2D

CURRENT APPLICATION NUMBER: US/09/808,037

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/629,971

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/473,653

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: US 60/152,417

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.0

SEQ ID NO 19

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic peptide

US-09-808-037-19

Query Match 89.6%; Score 43; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
|||||

Db 2 QRSSYPFT 9

Search completed: December 23, 2002, 07:58:19
Job time : 0.837209 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 0.889535 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	37	77.1	1501	1	NINC_DROME	P10676 drosophila
2	35	72.9	108	1	KV1V_HUMAN	P04430 homo sapien
3	34	70.8	108	1	KV1_CANFA	P01618 canis famil
4	34	70.8	275	1	CHRL_VIBCH	Q9kq06 vibrio chol
5	34	70.8	341	1	HEAD_LAMBD	P03713 bacterioph
6	34	70.8	343	1	CYS1_DICDI	P04988 dictyosteli
7	33	68.8	108	1	KV1L_HUMAN	P01604 homo sapien
8	33	68.8	345	1	YDE9_SCHPO	Q10442 schizosacch
9	33	68.8	556	1	PPBD_BACSU	P42251 bacillus su
10	33	68.8	662	1	YLN9_CAEEL	Q09512 caenorhabdi
11	32	66.7	265	1	TF2D_STRPU	P91809 strongyloce
12	32	66.7	446	1	CN7B_MOUSE	Q9qxq1 mus musculu
13	32	66.7	450	1	CN7B_HUMAN	Q9np56 homo sapien
14	32	66.7	872	1	SCD5_YEAST	P34758 saccharomyc
15	32	66.7	1476	1	AT7A_CRIGR	P49015 cricetulus
16	31	64.6	129	1	KV4A_MOUSE	P01680 mus musculu
17	31	64.6	275	1	CHER_VIBAN	Q57508 vibrio angu
18	31	64.6	275	1	CHER_VIBPA	Q9x9k2 vibrio para
19	31	64.6	360	1	CHLI_MESVI	Q9mut3 mesostigma
20	31	64.6	398	1	KYE1_KLULA	P40952 kluyveromyc
21	31	64.6	588	1	CMC2_CAEEL	Q20799 caenorhabdi
22	31	64.6	673	1	FXO3_HUMAN	O43524 homo sapien
23	31	64.6	750	1	PTP2_YEAST	P29461 saccharomyc
24	31	64.6	891	1	MAZ3_SCHCO	P37937 schizophyil
25	31	64.6	1115	1	DP3A_BACSU	O34623 bacillus su
26	30	62.5	118	1	YMX2_YEAST	Q04276 saccharomyc
27	30	62.5	268	1	Y145_METJA	Q57609 methanococc
28	30	62.5	313	1	VU47_HSV7J	P52525 human herpe
29	30	62.5	317	1	YRC3_CAEEL	Q10042 caenorhabdi
30	30	62.5	329	1	YHO3_YEAST	P14693 saccharomyc
31	30	62.5	376	1	CYS2_DICDI	P04989 dictyosteli
32	30	62.5	380	1	CYB_HUMAN	P00156 homo sapien
33	30	62.5	396	1	REPA_BACSU	P13962 bacillus su

34	30	62.5	396	1	VE2_HP48	Q80923 human papil
35	30	62.5	403	1	IF4A_LEIBR	Q25225 leishmania
36	30	62.5	442	1	CYS4_DICDI	P54639 dictyosteli
37	30	62.5	478	1	VP26_DROME	Q9w552 drosophila
38	30	62.5	658	1	CNT2_HUMAN	O43868 homo sapien
39	30	62.5	726	1	YE40_MYCPN	P75338 mycoplasma
40	30	62.5	865	1	FLUG_EMENI	P38094 emericeella
41	30	62.5	928	1	DNLI_CANAL	P52496 candida alb
42	30	62.5	1072	1	SYIC_YEAST	P09436 saccharomyc
43	30	62.5	1106	1	ACLY_CAEEL	P53585 caenorhabdi
44	30	62.5	1487	1	MDS3_YEAST	P53094 saccharomyc
45	30	62.5	1516	1	NCO2_XENLA	Q9w705 xenopus lae

ALIGNMENTS

RESULT 1
NINC_DROME STANDARD; PRT; 1501 AA.
AC P10676; P10677;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neither inactivation nor afterpotential protein C (EC 2.7.1.37).
GN NINAC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RX MEDLINE=88151067; PubMed=2449973;
RA Montell C., Rubin G.M.;
RT "The Drosophila ninaC locus encodes two photoreceptor cell specific
RT proteins with domains homologous to protein kinases and the myosin
RT heavy chain head.";
RL Cell 52:757-772(1988).
CC -!- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC
CC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN
CC ACTIVITIES.
CC -!- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: CYTOSKELETON.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC short form; are produced by alternative splicing.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SER/THR
CC FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN
CC SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03131; AAA28718.1; -.
CC EMBL; J03131; AAA28719.1; -.
CC EMBL; M20230; AAA28721.1; -.
CC EMBL; M20231; AAA28720.1; -.
CC PIR; A29813; A29813.
CC PIR; B29813; B29813.
CC HSSP; P08799; 1MND.
CC FlyBase; FBgn0002938; ninaC.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR000048; IQ_region.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR001609; myosin_head.
CC Pfam; PF00063; myosin_head; 1.
CC -----

DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00612; IQ; 2.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 2.
DR PROSITE; PS00096; IQ; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Cytoskeleton; Actin-binding; ATP-binding; Myosin; Transferase; Vision;
KW Serine/threonine-protein kinase; Alternative splicing.
FT DOMAIN 16 282 PROTEIN KINASE.
FT DOMAIN 335 1035 MYOSIN.
FT DOMAIN 1036 1065 IQ.
FT DOMAIN 1066 1501 NON ALPHA-HELICAL, C-TERMINAL DOMAIN.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT DOMAIN 913 934 ACTIN-BINDING (BY SIMILARITY).
FT VARSPLIC 1082 1135 AFRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKS
FT FQVLLHYRAARF -> GKTKQVDRRLREYDEEHIDISETPS
FT EAEEMFLEARMDEALAAVRIAKIEQASAE (IN SHORT ISOFORM).
FT VARSPLIC 1136 1501 MISSING (IN SHORT ISOFORM).
FT CONFLICT 253 253 K -> Q (IN REF. 1; AAA28720/AAA28721).
FT CONFLICT 1089 1089 P -> R (IN REF. 1; AAA28721).
SQ SEQUENCE 1501 AA; 174269 MW; D167EABC82A3933A CRC64;

Query Match 77.1%; Score 37; DB 1; Length 1501;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYP 7
Db 1352 QQRSSYP 1358

RESULT 2
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet E.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSSP; P80362; LWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 89 QQYNSYPFT 97

RESULT 3
KV1_CANFA
ID KV1_CANFA STANDARD; PRT; 108 AA.
AC P01618;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region GOM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a canine myeloma immunoglobulin: evidence that the VK subgroups predated mammalian speciation.";
RT Immunochimistry 15:303-305(1978).
CC -!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR; A01907; K2DGGM.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QQRSSYPFT 9
Db 90 QRSFYPT 97

RESULT 4
CHRL_VIBCH
ID CHRL_VIBCH STANDARD; PRT; 275 AA.
AC Q9KQ06; Q9XCL5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chemotaxis protein methyltransferase 1 (EC 2.1.1.80).
GN CHER1 OR CHER OR VC2201.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]


```
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN [2]
RP SEQUENCE OF 10-266 FROM N.A.
RC STRAIN=CVD110;
RX MEDLINE=99328977; PubMed=10400589;
RA O'Toole R., Lundberg S., Fredriksson S.A., Jansson A., Nilsson B.,
RA Wolf-Watz H.;
RT "The chemotactic response of Vibrio anguillarum to fish intestinal
RT mucus is mediated by a combination of multiple mucus components.";
RL J. Bacteriol. 181:4308-4317(1999).
CC -!- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER
CC RESIDUES IN MCP (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
CC = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC -!- SIMILARITY: CONTAINS 1 CHER-TYPE METHYLTRANSFERASE DOMAIN.
CC -----
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CC -----
CC EMBL; AE004291; AAF95346.1; -.
CC EMBL; AF139167; AAD45254.1; -.
CC HSSP; P07801; 1AF7.
CC TIGR; VC2201; -.
CC InterPro; IPR000780; Cher_Metranf.
CC InterPro; IPR001601; Methyltransf.
CC Pfam; PF01739; Cher; 1.
CC Pfam; PF03705; Cher_N; 1.
CC PRINTS; PR00996; CHERMTFRASE.
CC SMART; SM00138; Metrc; 1.
CC PROSITE; PS50123; CHER; 1.
CC transferase; Methyltransferase; Complete proteome.
KW DOMAIN 1 275 CHER-TYPE METHYLTRANSFERASE.
FT SEQUENCE 275 AA; 30871 MW; F008ADCBEA46A921 CRC64;
SQ
Query Match 70.8%; Score 34; DB 1; Length 275;
Best Local Similarity 85.7%; Pred. No. 8.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 RSSYPFT 9
Db 82 RDSYPFT 88
RESULT 5
HEAD_LAMBDA
ID HEAD_LAMBDA STANDARD; PRT; 341 AA.
AC P03713;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Major head protein (GPE) (Major coat protein).
GN E.
OS Bacteriophage lambda.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
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OX NCBI_TaxID=10710;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83189071; PubMed=62211115;
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RT "Nucleotide sequence of bacteriophage lambda DNA.";
RL J. Mol. Biol. 162:729-773(1982).
CC -!- FUNCTION: GENE E PROTEIN IS A MAJOR COMPONENT OF THE PHAGE HEAD.
CC THERE ARE ABOUT 420 COPIES OF PROTEIN E PER MATURE PHAGE. SOME OF
CC THE E PROTEIN IS COVALENTLY LINKED WITH AN EQUI-MOLAR AMOUNT OF
CC PROTEIN C AND CLEAVED TO YIELD MINOR CAPSID PROTEINS X1 AND X2.
CC -!- SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF PHI-80 AND P21.
CC -----
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CC -----
CC EMBL; J02459; AAA96540.1; -.
CC PIR; A04335; VHBPEL.
KW Coat protein.
SQ SEQUENCE 341 AA; 38188 MW; 31C50E4B38DA44A9 CRC64;
Query Match 70.8%; Score 34; DB 1; Length 341;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 RSSYPFT 9
Db 29 RESYPFT 35
RESULT 6
CYSL_DICDI
ID CYSL_DICDI STANDARD; PRT; 343 AA.
AC P04988;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine proteinase 1 precursor (EC 3.4.22.-).
GN CPRA OR CP1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85257519; PubMed=2990918;
RA Williams J.G., North M.J., Mahubani H.M.;
RT "A developmentally regulated cysteine proteinase in Dictyostelium
RT discoideum.";
RL EMBO J. 4:999-1006(1985).
RN [2]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=96210028; PubMed=8631906;
RA Mehta D.P., Ichikawa M., Salimath P.V., Etchison J.R., Haak R.,
RA Manzi A., Freeze H.H.;
RT "A lysosomal cysteine proteinase from Dictyostelium discoideum
RT contains N-acetylglucosamine-1-phosphate bound to serine but not
RT mannose-6-phosphate on N-linked oligosaccharides.";
RL J. Biol. Chem. 271:10897-10903(1996).
CC -!- FUNCTION: CYSTEINE PROTEINASES 1 AND 2 ARE BELIEVED TO PARTICIPATE
CC IN THE BREAKDOWN OF PROTEIN DURING DIFFERENTIATION OF
CC DICTYOSTELIUM AS A RESPONSE TO STARVATION.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- PTM: PHOSPHOGLYCOSYLATED, CONTAINS GLCNAC-ALPHA-1-P-SER RESIDUES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC -----
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DR EMBL; X02407; CAA26255.1; -
DR PIR; A22827; KHDO.
DR HSSP; P25779; IAIM.
DR MEROPS; C01.0PA; -
DR GlycoSuiteDB; P04988; -
DR SWISS-2DPAGE; P04988; DICTY.
DR DictyDb; DD02003; cpra.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00139; THIOLEPROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOLEPROTEASE_HIS; 1.
DR PROSITE; PS00640; THIOLEPROTEASE_ASN; 1.
KW Hydrolase; Thiol protease; Lysosome; Zymogen; Glycoprotein;
KW Phosphorylation; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 117 ACTIVATION PEPTIDE.
FT CHAIN 118 343 CYSTEINE PROTEINASE 1.
FT ACT_SITE 142 142 BY SIMILARITY.
FT ACT_SITE 286 286 BY SIMILARITY.
FT ACT_SITE 311 311 BY SIMILARITY.
FT DISULFID 139 190 BY SIMILARITY.
FT DISULFID 173 224 BY SIMILARITY.
FT DISULFID 279 332 BY SIMILARITY.
SQ SEQUENCE 343 AA; 38495 MW; 71804C15F2B361E2 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 343;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 209 QTESSYPFT 217

RESULT 7
KVIL_HUMAN
ID KVIL_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RT sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01870; K1HKUK.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 5.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 89 QQYSRYPYT 97

RESULT 8
YDE9_SCHPO
ID YDE9_SCHPO STANDARD; PRT; 345 AA.
AC Q10442;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative mitochondrial carrier C12B10.09.
GN SPAC12B10.09.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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CC EMBL; 270721; CAA94699.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KW Transmembrane; Transp.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 83 103 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
FT TRANSMEM 296 316 POTENTIAL.
FT TRANSMEM 319 339 POTENTIAL.
SQ SEQUENCE 345 AA; 38451 MW; 39081A6AAC984B2C CRC64;

Query Match 68.8%; Score 33; DB 1; Length 345;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
   ||| || ||
Db 290 QORLSYVFT 298

RESULT 9
PPBD_BACSU
ID PPBD_BACSU STANDARD; PRT; 556 AA.
AC P42251;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alkaline phosphatase D precursor (EC 3.1.3.1) (APASED) (RAN1) (BC6).
GN PHOD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 57-76.
RC STRAIN=168 / JH642;
RX MEDLINE=96349109; PubMed=8760916;
RA Eder S., Shi L., Jensen K., Yamane K., Hulett F.M.;
RT "A Bacillus subtilis secreted phosphodiesterase/alkaline phosphatase
is the product of a pho regulon gene, phoD.";
RL Microbiology 142:2041-2047(1996).
RN [2]
RP SEQUENCE OF 95-556 FROM N.A.
RC STRAIN=168;
RX MEDLINE=95219079; PubMed=7704254;
RA Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
RT "Determination of a 21548 bp nucleotide sequence around the 24
degrees region of the Bacillus subtilis chromosome.";
RL Microbiology 141:269-275(1995).
RN [3]
RP CHARACTERIZATION.
RC STRAIN=6060-BC6;
RX MEDLINE=78171419; PubMed=25878;
RA Yamane K., Maruo B.;
RT "Purification and characterization of extracellular soluble and
membrane-bound insoluble alkaline phosphatases possessing
phosphodiesterase activities in Bacillus subtilis.";
RL J. Bacteriol. 134:100-107(1978).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC , alcohol + phosphate.
CC -!- INDUCTION: BY PHOSPHATE STARVATION.
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CC EMBL; U49060; AAB47803.1; -.
DR EMBL; D30808; BAA06483.1; -.
DR EMBL; Z99105; CAB12056.1; -.
DR Subtilist; BGL1174; phoD.
KW Hydrolase; Signal; Complete proteome.
KW SIGNAL 1 56
FT CHAIN 57 556 ALKALINE PHOSPHATASE D.
FT VARIANT 59 59 N -> K.
SQ SEQUENCE 556 AA; 62829 MW; 125F7FDDA08817E3 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSSYPFT 9
   |||||
Db 61 SSSYPFT 66

RESULT 10
YLN9_CAEEL
ID YLN9_CAEEL STANDARD; PRT; 662 AA.
AC Q09512;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical 76.7 kDa protein D2013.9 in chromosome II.
GN D2013.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Mortimore B., Matthews P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 TTL DOMAIN.
-----
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```

```
-----
CC EMBL; Z47808; CAA87778.1; -.
DR EMBL; Z47809; CAA87778.1; JOINED.
DR EMBL; Z47809; CAA87783.1; -.
DR EMBL; Z47808; CAA87783.1; JOINED.
DR WormPep; D2013.9; CE01535.
DR InterPro; IPR001214; SET.
DR InterPro; IPR004344; Tub_tyr_lygase.
DR Pfam; PF03133; TTL; 1.
DR PROSITE; PS50280; SET; 1.
KW Hypothetical protein.
FT DOMAIN 209 260 SET.
FT DOMAIN 370 662 TTL.
SQ SEQUENCE 662 AA; 76750 MW; 5044C76422145698 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 662;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
   : |||:
Db 3 EDRSAYPFS 11

RESULT 11
```

```
TF2D_STRPU
ID TF2D_STRPU STANDARD; PRT; 265 AA.
AC P91809;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription initiation factor TFIID (TATA-box factor)
DE (TATA sequence-binding protein) (TBP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Rybacki L., Childs G.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
CC OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
CC SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
CC THE POSITION OF TRANSCRIPTION INITIATION.
CC -!- SUBUNIT: BINDS DNA AS A MONOMER.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE TBP FAMILY.
CC -----
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CC -----
DR EMBL; U86586; AAB47272.1; -.
DR HSSP; P20226; ITGH.
DR InterPro; IPR000814; TFIID.
DR Pfam; PF00352; TBP; 2.
DR PRINTS; IPR00686; TIFACTORIID.
DR PROSITE; PS00351; TFIID; 2.
KW Transcription regulation; DNA-binding; Nuclear protein; Repeat.
FT REPEAT 91 167
FT REPEAT 181 258
FT REPEAT 265 291
SQ SEQUENCE 265 AA; 29107 MW; 53AED314D2D98926 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 265;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYP 7
Db 23 QORSHYP 29
||| ||
||| ||

RESULT 12
CN7B_MOUSE
ID CN7B_MOUSE STANDARD; PRT; 446 AA.
AC Q9QXQ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087273; PubMed=10618442;
RA Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT "Cloning and characterization of PDE7B, a cAMP-specific
RT phosphodiesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
```

```
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT cAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC -!- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF190639; AAF25195.1; -.
DR EMBL; AJ251859; CAB92530.1; -.
DR MGD; MGI:1352752; Pde7b.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP.
FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5A8 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 446;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPF 8
Db 41 ERRGSYPF 48
::| ||||
||| |||

RESULT 13
CN7B_HUMAN
ID CN7B_HUMAN STANDARD; PRT; 450 AA.
AC Q9NP56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20275458; PubMed=10814504;
RA Sasaki T., Kotera J., Yuasa K., Omori K.;
RT "Identification of human PDE7B, a cAMP-specific phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
RN [2]
```


RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT cAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. ALSO EXPRESSED IN
CC HEART, LIVER, SKELETAL MUSCLE AND PANCREAS.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AB038040; BAA96537.1; -.
DR EMBL; AJ251860; CAB92441.1; -.
DR Genew; HGNC:8792; PDE7B.
DR MIM; 604645; -.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP.
FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 450;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPF 8
Db 41 ERRGSYPF 48
::: |||||

RESULT 14
SCD5_YEAST STANDARD; PRT; 872 AA.
AC P34758;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SCD5 protein (FTB1 protein).
GN SCD5 OR FTB1 OR YOR329C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX PubMed=8688556;
RA Nelson K.K., Holmer M., Lemmon S.K.;
RT "SCD5, a suppressor of clathrin deficiency, encodes a novel protein
RT with a late secretory function in yeast.";

RL Mol. Biol. Cell 7:245-260(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Wang W., Zheng L., Chan C.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RA Song J.M., Cheung E., Rabinowitz J.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051586; PubMed=8896263;
RA Parle-Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
RT "Sequence of 29 kb around the PDR10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I.";
RL yeast 12:999-1004(1996).
CC -!- FUNCTION: Involved in vesicular transport at a late stage of the
CC secretory pathway.
CC -!- SUBUNIT: PUTATIVE 10-FORMYL-TETRAHYDROFOLATE BINDING PROTEIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -----
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CC -----
DR EMBL; U03492; AAB09719.1; -.
DR EMBL; U42227; AAA85443.1; -.
DR EMBL; Z49821; CAA89976.1; -.
DR EMBL; Z75237; CAA99650.1; -.
DR SGD; S0005856; SCD5.
KW Transport; Protein transport; Membrane; Repeat.
FT DOMAIN 405 448 3 X 20 AA APPROXIMATE REPEATS.
FT REPEAT 405 424 1-1.
FT REPEAT 439 458 1-2.
FT REPEAT 479 498 1-3.
FT DOMAIN 534 728 9 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 534 545 2-1.
FT REPEAT 564 575 2-2.
FT REPEAT 593 604 2-3.
FT REPEAT 608 619 2-4.
FT REPEAT 623 634 2-5.
FT REPEAT 636 647 2-5.
FT REPEAT 650 661 2-7.
FT REPEAT 683 694 2-8.
FT REPEAT 717 728 2-9.
SQ SEQUENCE 872 AA; 97305 MW; C60F5BE8808E1D31 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 872;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPF 9
Db 831 QQQQQFPFT 839
::: |||||

RESULT 15
AT7A_CRIGR STANDARD; PRT; 1476 AA.
ID AT7A_CRIGR
AC P49015;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Copper-transporting ATPase 1 (EC 3.6.3.4) (Copper pump 1)
DE (Fragment).
GN ATP7A.

OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K16
RX MEDLINE=960154683; PubMed=8589689;
RA Camakaris J., Petris M.J., Bailey L., Shen P., Lockhart P.,
RA Glover T.W., Barcroft C., Patton J., Mercer J.F.;
RT "Gene amplification of the Menkes (MNK; ATP7A) P-type ATPase gene of
RT CHO cells is associated with copper resistance and enhanced copper
RT efflux."
RL Hum. Mol. Genet. 4:2117-2123(1995).
CC -!- FUNCTION: MAY FUNCTION IN THE EXPORT OF COPPER FROM THE CYTOPLASM
CC TO AN INTRACELLULAR ORGANELLE. IT MAY SERVE AS WELL FOR THE EXPORT
CC OF OTHER METALS.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+)(In) = ADP + phosphate +
CC Cu(2+) (Out).
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: FOUNDS IN MOST TISSUES EXCEPT LIVER.
CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES).
CC -!- SIMILARITY: CONTAINS 6 HMA DOMAINS.
CC -----
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CC -----
DR EMBL; U29946; AAB39918.1; -.
DR HSSP; O04656; LAW0.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR001934; HeavyMe_transpt.
DR InterPro; IPR001454; Hlgnase/hydrase.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00403; HMA; 6.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMS; TIGR00003; HMA; 6.
DR PROSITE; PS00154; ATPase_E1_E2; 1.
DR PROSITE; PS01047; HMA_1; 5.
DR PROSITE; PS50846; HMA_2; 6.
KW Hydrolase; Copper transport; Transmembrane; Phosphorylation;
KW ATP-binding; Metal-binding; Copper; Repeat.
FT DOMAIN 1 642
FT TRANSMEM 643 665 POTENTIAL.
FT TRANSMEM 695 717 POTENTIAL.
FT TRANSMEM 736 760 POTENTIAL.
FT TRANSMEM 770 788 POTENTIAL.
FT TRANSMEM 930 952 POTENTIAL.
FT TRANSMEM 978 998 POTENTIAL.
FT TRANSMEM 1347 1373 POTENTIAL.
FT TRANSMEM 1379 1397 POTENTIAL.
FT DOMAIN 9 75 HMA 1.
FT DOMAIN 172 238 HMA 2.
FT DOMAIN 277 343 HMA 3.
FT DOMAIN 377 443 HMA 4.
FT DOMAIN 479 545 HMA 5.
FT DOMAIN 555 621 HMA 6.
FT MOD_RES 1034 1034 PHOSPHORYLATION (PROBABLE).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 685 685 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 887 887 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 953 953 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1130 1130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1134 1134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 1476 1476

SQ SEQUENCE 1476 AA; 160335 MW; 6B36F5A2AC358C0B CRC64;
Query Match 66.7%; Score 32; DB 1; Length 1476;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QORSSYP 7
Db 267 QORPSYP 273
Search completed: December 23, 2002, 07:26:10
Job time : 2.88953 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 3.73256 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	38	79.2	134	11	Q8VDD0	Q8vdd0 mus musculu
2	37	77.1	106	5	Q9U410	Q9u410 schistosoma
3	37	77.1	269	5	Q18582	Q18582 caenorhabdi
4	37	77.1	289	13	Q8UUZ5	Q8uuz5 brachydanio
5	36	75.0	886	16	Q9KC72	Q9kc72 bacillus ha
6	35	72.9	108	11	Q8VIJ0	Q8vij0 mus musculu
7	35	72.9	133	3	Q12744	Q12744 saccharomyc
8	34	70.8	341	16	Q8X6Y8	Q8x6y8 escherichia
9	34	70.8	363	10	Q9SWC7	Q9swc7 glycine max
10	34	70.8	377	10	Q24324	Q24324 phaseolus v
11	34	70.8	380	10	Q43448	Q43448 glycine max
12	34	70.8	393	5	O96635	O96635 trypanosoma
13	34	70.8	397	16	O35007	O35007 bacillus su
14	34	70.8	399	16	Q9K6Q6	Q9k6q6 bacillus ha
15	34	70.8	478	5	O96750	O96750 trypanosoma
16	34	70.8	653	3	Q12171	Q12171 saccharomyc

17	34	70.8	721	16	Q99YL1	Q99yl1 streptococc
18	34	70.8	977	5	O97357	O97357 trypanosoma
19	34	70.8	1138	16	Q92KB6	Q92kb6 rhizobium m
20	34	70.8	1194	5	Q9VSI2	Q9vsi2 drosophila
21	33	68.8	169	5	Q8SVY7	Q8svy7 encephalito
22	33	68.8	234	11	Q8R062	Q8r062 mus musculu
23	33	68.8	246	13	Q9W6E5	Q9w6e5 gallus gall
24	33	68.8	380	3	Q9P8H2	Q9p8h2 cryptococcu
25	33	68.8	434	5	Q94503	Q94503 dictyosteli
26	33	68.8	539	5	Q9V490	Q9v490 drosophila
27	33	68.8	543	5	Q961N4	Q961n4 drosophila
28	33	68.8	543	5	Q9XZC2	Q9xzc2 drosophila
29	33	68.8	580	10	Q9SIY8	Q9siy8 arabidopsis
30	33	68.8	685	16	Q92TJ0	Q92tj0 rhizobium m
31	33	68.8	733	13	Q91817	Q91817 xenopus lae
32	33	68.8	1108	5	Q8T2E2	Q8t2e2 dictyosteli
33	33	68.8	3232	3	O94205	O94205 claviceps p
34	32	66.7	196	5	Q9VD29	Q9vdz9 drosophila
35	32	66.7	210	5	Q95SL8	Q95sl8 drosophila
36	32	66.7	210	5	Q9W3R3	Q9w3r3 drosophila
37	32	66.7	237	5	Q8SXD8	Q8sxd8 drosophila
38	32	66.7	250	17	Q8TIX4	Q8tix4 methanosarc
39	32	66.7	271	5	O77208	O77208 lytechinus
40	32	66.7	374	2	O69413	O69413 escherichia
41	32	66.7	374	16	O85626	O85626 escherichia
42	32	66.7	412	12	Q8QRX0	Q8qrx0 chimpanzee
43	32	66.7	422	4	Q9B240	Q9bz40 homo sapien
44	32	66.7	428	5	Q8SXA2	Q8sxa2 drosophila
45	32	66.7	446	11	Q8VIE4	Q8vie4 rattus norv

ALIGNMENTS

RESULT 1
Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chernaiovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Sembi P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;

Query Match 79.2%; Score 38; DB 11; Length 134;
Best Local Similarity 87.5%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 QRSSYPFT 9

Db 111 QRSSYPWT 118
|||||:|
RESULT 2
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 77.1%; Score 37; DB 5; Length 106;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPPT 9
||:|||||
Db 88 QQWTSYPPT 96

RESULT 3
Q18582
ID Q18582 PRELIMINARY; PRT; 269 AA.
AC Q18582;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 30.8 kDa protein.
GN C42D8.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Hallsworth K.;
RT "The sequence of C. elegans cosmid C42D8.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;

RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U56966; AAA98721.2; -.
KW Hypothetical protein.
SQ SEQUENCE 269 AA; 30847 MW; 32D2B7A1C0102F93 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 269;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPPT 9
|:|:|||||
Db 225 QRRENYPT 233

RESULT 4
Q8UUZ5
ID Q8UUZ5 PRELIMINARY; PRT; 289 AA.
AC Q8UUZ5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Orthodenticle-related homeobox 5.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21624608; PubMed=11753388;
RA Gamse J.T., Liang J.O., Shen Y.-C., Raymond P., Thisse B., Thisse C.,
RA Halpern M.E.;
RT "Otx5 regulates genes that show circadian expression in the zebrafish
RT pineal complex.";
RL Nat. Genet. 30:117-121(2002).
DR EMBL; AY036005; AAK62029.1; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_repressr.
DR InterPro; IPR003025; Otx_TF.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF03529; TF_Otx; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRINTS; PR01255; OTXHOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 289 AA; 31422 MW; 542FA0F69AE90DAC CRC64;

Query Match 77.1%; Score 37; DB 13; Length 289;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPPT 9
|||||:|
Db 177 QRSSYPMT 184

RESULT 5
Q9KC72
ID Q9KC72 PRELIMINARY; PRT; 886 AA.
AC Q9KC72;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Penicillin-binding proteins 1A/1B.
GN PONA OR BH1702.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

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OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05421.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001264; GT_51.
DR InterPro; IPR001460; Transpeptdse.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00912; Transglycosyl; 1.
DR Pfam; PF00905; Transpeptidase; 1.
DR ProDom; PD001895; GT_51; 1.
DR SMART; SM00060; FN3; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 886 AA; 98280 MW; 0662807F75148534 CRC64;

Query Match 75.0%; Score 36; DB 16; Length 886;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPF 8
Db 282 QERESYPF 289
|:| ||||

RESULT 6
Q8VIJ0
ID Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VK19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ-LPR/LPR;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 72.9%; Score 35; DB 11; Length 108;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 89 QQYNSYPYT 97
||:|||||
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RESULT 7
Q12744
ID Q12744 PRELIMINARY; PRT; 133 AA.
AC Q12744;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical ORF IDENTICAL to ORF NOTED in RAD10 5' region A22726.
GN YML095C-A.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Gentles S., Bowman S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Barrell B., Rajandream M.A.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 2-133 FROM N.A.
RX MEDLINE=85284950; PubMed=3896774;
RA Weiss W.A., Friedberg E.C.;
RT "Molecular cloning and characterization of the yeast RAD10 gene and
RT expression of RAD10 protein in E. coli.";
RL EMBO J. 4:1575-1582(1985).
DR EMBL; Z46660; CAA86643.1; -.
DR EMBL; X02591; CAA26432.1; -.
DR SGD; S0004561; YML095C-A.
DR InterPro; IPR002016; Peroxidase.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWNL1.
SQ SEQUENCE 133 AA; 15007 MW; B93007588867456 CRC64;

Query Match 72.9%; Score 35; DB 3; Length 133;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 101 QQRRSYSFT 109
||| ||||

RESULT 8
Q8X6Y8
ID Q8X6Y8 PRELIMINARY; PRT; 341 AA.
AC Q8X6Y8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative capsid protein of prophage CP-933X (Putative major capsid
DE protein).
GN Z1888 OR ECS2174 OR ECS1635.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Groetbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
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[2]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21556231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL; AE005330; AAG55985.1; -.
EMBL; AP002557; BAB35597.1; -.
EMBL; AP002555; BAB35058.1; -.
Complete proteome.
SEQUENCE 341 AA; C0310C4DE97C0037 CRC64;

Query Match 70.8%; Score 34; DB 16; Length 341;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPT 9
| | | | |
Db 29 RESYPT 35

RESULT 9
Q9SWC7 PRELIMINARY; PRT; 363 AA.
ID Q9SWC7
AC Q9SWC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative cysteine proteinase GMPM33.
GN GMPM33.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1].
SEQUENCE FROM N.A.
STRAIN=CV. SHI-SHI;
Chow T.Y., Liu S.M., Lin T.Y., Hsing Y.I.C.;
"Characterization of soybean seed maturation protein, PM33.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; A067986; AAD46920.1; -.
HSSP; P25779; IAIM.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase_C1; 1.
PROSITE; PS00640; THIOI_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW Hydrolase; Thiol protease.
SEQUENCE 363 AA; 39685 MW; 55C46B8F2CAC8EFB CRC64;

Query Match 70.8%; Score 34; DB 10; Length 363;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPPT 9
:: | | | | |
Db 213 EEESYPPT 221

RESULT 10
O24324 PRELIMINARY; PRT; 377 AA.
ID O24324
AC O24324;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cysteine proteinase precursor.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1].
SEQUENCE FROM N.A.
STRAIN=CV. MOLDAVIAN; TISSUE=COTYLEDON;
Senyuk V., Becker C., Muentz K.;
"Isolation of cDNA clone encoding cysteine proteinase (CP4) from a
cotyledon-specific cDNA library of germinating kidney bean seeds.";
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
EMBL; Z99955; CAB17077.1; -.
HSSP; P25779; IAIM.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase_C1; 1.
PROSITE; PS00640; THIOI_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
KW Hydrolase; Signal; Thiol protease.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 138 377 CYSTEINE PROTEINASE.
SQ SEQUENCE 377 AA; 41827 MW; 6576DEF3F1B26DA9 CRC64;

Query Match 70.8%; Score 34; DB 10; Length 377;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPPT 9
:: | | | | |
Db 228 EEESYPPT 236

RESULT 11
Q43448 PRELIMINARY; PRT; 380 AA.
ID Q43448
AC Q43448;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cysteine proteinase precursor.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1].
SEQUENCE FROM N.A.
STRAIN=CV. FISKEY V; TISSUE=COTYLEDON;
MEDLINE=95260869; PubMed=7742372;
Nong V., Becker C., Muentz K.;
"cdNA cloning for a putative cysteine proteinase from developing seeds
of soybean.";
Biochim. Biophys. Acta 1261:435-438(1995).
EMBL; Z32795; CAA83673.1; -.
HSSP; P25779; IAIM.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase_C1; 1.
PROSITE; PS00640; THIOI_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW Hydrolase; Signal; Thiol protease.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 140 380 CYSTEINE ENDOPEPTIDASE.
SQ SEQUENCE 380 AA; 41590 MW; 902A93F8132D56C1 CRC64;

Query Match 70.8%; Score 34; DB 10; Length 380;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
:: |||||
Db 230 EESSYPYT 238

RESULT 12
O96635 PRELIMINARY; PRT; 393 AA.
AC O96635;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Lysosomal alpha mannosidase (Fragment).
GN O20.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL BRENER;
RX MEDLINE=20160916; PubMed=10688909;
RA Vazquez M.P., Ben-Dov C.P., Lorenzi H.A., Moore T., Schijman A.G.,
RA Levin M.J.;
RT "The short interspersed repetitive element of Trypanosoma cruzi, SIRE,
RT is associated to VIPER, a novel and unusual retroelement related to
RT LTR-retrotransposons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2128-2133(2000).
DR EMBL; AF096926; AAC72969.1; -.
FT NON_TER 1
SQ SEQUENCE 393 AA; 44188 MW; A728125DDA5CA282 CRC64;

Query Match 70.8%; Score 34; DB 5; Length 393;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPFT 9
|| ||||
Db 147 RSDYPFT 153

RESULT 13
O35007 PRELIMINARY; PRT; 397 AA.
AC O35007;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE YVRP protein.
GN YVRP.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Wipat A., Brignell C.S., Guy J.B., Rose M., Emmerson P.T.,
RA Harwood C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 4-397 FROM N.A.
RC STRAIN=168;
RA Rose M., Entian K.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Harwood D.R.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99120; CAB15319.1; -.
DR EMBL; Z99121; CAB15334.1; -.
DR EMBL; AJ223978; CAA11723.1; -.
KW Complete proteome.
SQ SEQUENCE 397 AA; 43492 MW; 9FBF8280458AD7CF CRC64;

Query Match 70.8%; Score 34; DB 16; Length 397;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
| | : |||
Db 288 QSSNYPFT 295

RESULT 14
Q9K6Q6 PRELIMINARY; PRT; 399 AA.
ID Q9K6Q6
AC Q9K6Q6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ABC transporter.
GN BH3672.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07391.1; -
KW Complete proteome.
SQ SEQUENCE 399 AA; 45051 MW; 4FA5D772A8D3960C CRC64;

Query Match 70.8%; Score 34; DB 16; Length 399;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
| | | | |
Db 287 QSSNYPFT 294

RESULT 15
O96750 PRELIMINARY; PRT; 478 AA.
AC O96750;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ESAG5 protein.
GN ESAG5.
OS Trypanosoma brucei rhodesiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID-31286;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EATRO 3;
RX MEDLINE=99081299; PubMed=9865701;
RA Xong H.V., Vanhamme L., Chamekh M., Chimfwembe E.C.,
RA Van den Abbeele J., Pays A., van Meirvenne N., Hamers R.,
RA de Batselier P., Pays E.;
RT "A VSG expression site-associated gene confers resistance to human
RL serum in Trypanosoma rhodesiens.";
RL Cell 95:839-846(1998).
DR EMBL; AJ010094; CAA09000.1; -
SQ SEQUENCE 478 AA; 52703 MW; 3CC5004781E5B97F CRC64;

Query Match 70.8%; Score 34; DB 5; Length 478;
Best Local Similarity 87.5%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
| | | | |
Db 28 QRSSSPFT 35

Search completed: December 23, 2002, 07:29:54
Job time : 5.73256 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 21.0872 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-7
Perfect score: 631
Sequence: 1 QVKLQSGAELVGSASVKL.....AAYGDYEGYWGQGTTRVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB	ID	Description
1	554.5	87.9		535	4	US-08-983-035A-38	Sequence 38, Appl
2	532.5	84.4		118	3	US-08-767-128-22	Sequence 22, Appl
3	513.5	81.4		270	2	US-08-652-507-2	Sequence 2, Appl
4	507.5	80.4		124	1	US-08-017-570-6	Sequence 6, Appl
5	507.5	80.4		124	1	US-08-471-426-6	Sequence 6, Appl
6	507.5	80.4		124	5	PCT-US94-01709-6	Sequence 6, Appl
7	507.5	80.4		553	2	US-08-661-052-16	Sequence 16, Appl
8	507.5	80.4		553	4	US-09-188-082-16	Sequence 16, Appl
9	507.5	80.4		553	4	US-09-364-088-16	Sequence 16, Appl
10	507.5	80.4		553	4	US-09-102-716-16	Sequence 16, Appl
11	502.5	79.6		124	1	US-08-017-570-4	Sequence 4, Appl
12	502.5	79.6		124	1	US-08-471-426-4	Sequence 4, Appl
13	502.5	79.6		124	5	PCT-US94-01709-4	Sequence 4, Appl
14	499.5	79.2		124	4	US-09-672-609-1	Sequence 1, Appl
15	499.5	79.2		124	4	US-09-025-403A-1	Sequence 1, Appl
16	498.5	79.0		281	4	US-09-423-439-44	Sequence 44, Appl
17	498.5	79.0		642	4	US-09-423-439-26	Sequence 26, Appl
18	498.5	79.0		666	4	US-09-423-439-51	Sequence 51, Appl
19	495.5	78.5		255	4	US-09-171-945-19	Sequence 19, Appl
20	481.5	76.3		136	4	US-08-348-548-8	Sequence 8, Appl
21	481.5	76.3		136	5	PCT-US95-15716-8	Sequence 8, Appl
22	480.5	76.1		120	4	US-09-171-945-11	Sequence 11, Appl
23	480	76.1		125	2	US-08-561-521-44	Sequence 44, Appl
24	480	76.1		125	5	PCT-US95-01219-44	Sequence 44, Appl
25	478	75.8		117	2	US-08-290-592E-18	Sequence 18, Appl
26	478	75.8		117	5	PCT-US95-10053-15	Sequence 15, Appl
27	478	75.8		117	5	PCT-US96-09448-18	Sequence 18, Appl

28	475	75.3	136	4	US-08-646-265A-29	Sequence 29, Appl
29	470.5	74.6	118	2	US-08-232-081B-38	Sequence 38, Appl
30	468	74.2	123	2	US-08-561-521-9	Sequence 9, Appl
31	468	74.2	123	5	PCT-US95-01219-9	Sequence 9, Appl
32	466	73.9	121	2	US-08-822-830B-13	Sequence 13, Appl
33	463	73.4	121	2	US-08-822-830B-2	Sequence 2, Appl
34	461	73.1	120	2	US-08-950-660-2	Sequence 2, Appl
35	461	73.1	120	5	PCT-US93-00030-2	Sequence 2, Appl
36	461	73.1	120	5	PCT-US93-00924-2	Sequence 2, Appl
37	460	72.9	140	2	US-08-561-521-4	Sequence 4, Appl
38	460	72.9	140	5	PCT-US95-01219-4	Sequence 4, Appl
39	458	72.6	136	1	US-08-024-253-2	Sequence 2, Appl
40	452	71.6	254	2	US-08-792-824-4	Sequence 4, Appl
41	452	71.6	254	2	US-08-792-824-7	Sequence 7, Appl
42	452	71.6	254	2	US-08-792-824-10	Sequence 10, Appl
43	452	71.6	254	2	US-08-792-824-13	Sequence 13, Appl
44	450.5	71.4	120	4	US-08-871-488A-15	Sequence 15, Appl
45	447.5	70.9	113	1	US-08-207-169A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-983-035A-38
; Sequence 38, Application US/08983035A
; Patent No. 6326464
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,035A
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01111
; FILING DATE: 17-JUL-1996
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Strauss, William L.
; REGISTRATION NUMBER: 47,114
; REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

Query Match 87.9%; Score 554.5; DB 4; Length 535;
Best Local Similarity 88.9%; Pred. No. 5.1e-48;

Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 3 QVQLQESGAELVSGASVKLSCTASGFNIKDYIMHWVKORPEQGLEWIGWIDPENGDTY 62
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTIVTVSS 117
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 APKFGKATMTADSSNTAYLQLSSLASEDTAVYCN-FYGDALDYWGQGTIVTVSS 118

RESULT 2

US-08-767-128-22
; Sequence 22, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-22

Query Match 84.4%; Score 532.5; DB 3; Length 118;
Best Local Similarity 85.6%; Pred. No. 1.4e-46;
Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
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Db 1 EVQLQSGAELVSRGASVKLSCTASGFNIKDYIMHWVKORPEQGLEWIGWIDPENGDTY 60
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAY-YGDYEGYWGQGTIVTVSS 117
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Db 61 DPKFGKATMTADTSSNIAYLQLSSLTSEDYAVYCNPNYGYDDAMDYWGQGTIVTVSS 118

RESULT 3

US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-507-2

Query Match 81.4%; Score 513.5; DB 2; Length 270;
Best Local Similarity 81.3%; Pred. No. 3e-44;
Matches 100; Conservative 4; Mismatches 10; Indels 9; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 QVKLQSGAELVSRGTSVKLSCTASGFNIKDSYMHVLRQPEQGLEWIGWIDPENGDTY 86
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCN-----AYGDYEGYWGQGTIVT 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 APKFGKATFTTDTSSNTAYLQLSSLTSEDYAVYCNNEGTPGPIYFD---YWGQGTIVT 143
QY 115 VSS 117
|||
Db 144 VSS 146

RESULT 4

US-08-017-570-6
; Sequence 6, Application US/08017570

```

; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-017-570-6

      Query Match      80.4%; Score 507.5; DB 1; Length 124
      Best Local Similarity 77.2%; Pred. No. 4.8e-44;
      Matches 98; Conservative 8; Mismatches 8; Indels 1

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPEN
Db 1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYIMHVVKQRPEQGLEWIGWIDPEN
QY 61 APKFGQKATMTADSSNTAYLQLSSLTSEDYAVYYCNA-----YYGDYEG
Db 61 APKFGQKATMTDTSSNTAYLQLSSLTSEDYAVYYCNRGLSTMITTRWFFD---
QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 5
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967

```

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; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-426-6

Query Match      80.4%; Score 507.5; DB 1; Length 124
Best Local Similarity 77.2%; Pred. No. 4.8e-44;
Matches 98; Conservative 8; Mismatches 8; Indels 1

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPEN
Db 1 EVQLQSGAELVRSASVKMSCTASGFNKIDYMHVVKORPEQGLEWIGWIDPEN
QY 61 APKFGKATMTADSSNTAYLQLSLSLTSEDYAVYCNA-----YYGDYEG
Db 61 APKFGKATMTDTSNTAYLQLSLSLTSEDYAVYCNTRGLSTMITTRWFFD---
QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 6
PCT-US94-01709-6
; Sequence 6, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-017096

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Query Match	80.4%	Score 507.5;	DB 5;	Length 124;
Best Local Similarity	77.2%;	Pred. No. 4.8e-44;		
Matches 98;	Conservative	8;	Mismatches 8;	Indels 13;
				Gaps 2;

Qy	1	QVKLQSGGAELVSGASVKLSCTTSGFNKIDFYMHVVKRPEQGLEWIGWIDPENGDSGY	60
		: H	
Db	1	EVQLQSGGAELVSRGASVKMSCTASGFNIKDYMHVVKRPEQGLEWIGWIDPENGDTGY	60
		: H	
Qy	61	APKQGGKATMTADSSNTAYLQLSLLTSEDYAVYYCNA-----YYGDYEGYWGQG	110
		H	
Db	61	APKQGGKATMTTDTSSNTAYLQLSLLTSEDYAVYYCNRGLSTMITTRWFFD---VWGAG	117
		: H	
Qy	111	TTTVTVSS	117
		H	
Db	118	TTTVTVSS	124

```

RESULT 7
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-661-052-16

Query Match	80.4%;	Score 507.5;	DB 2;	Length 553;
Best Local Similarity	80.3%;	Pred. No. 2.8e-43;		
Matches 98; Conservative	5;	Mismatches 10;	Indels 9;	Gaps 2;

QY	2	VKLQQGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIGWIDPENGDSGYA	61
Dd	278	IKLQQGAELVRSGTSVKLSCTFASGFNIKDSYMHWLRRGQPQGLEWIGWIDPENGDTGYA	337
QY	62	PKFQKGATMTADSSSNTAYLQLSSLTSEDTAIVYYCN-----AAYGDYEGYWGGQTTVTV	115
Dd	338	PKFQKGATFTTDTSSTNTAYLQLSSLTSEDTAIVYYCNEGTGPYYFD---YWGQGTTVTV	394
QY	116	SS 117	
Dd	395	SS 396	

```

RESULT 8
US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-16

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Query Match	80.4%;	Score 507.5;	DB 4;	Length 553;
Best Local Similarity	80.3%;	Pred. No. 2.8e-43;		
Matches 98; Conservative		5; Mismatches 10;	Indels 9;	Gaps 2;

Qy	2	VKLQQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWDPENGDGYA	61
		: : :	
Dd	278	IKLQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWDPENGDTEYA	337
Ov	62	PKFGSKATMTADSSSNTAYIOLSSLTSEDTAIVYC-----AYGDEYEGWGOGTTVTY	115

Db 338 PKFGKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPGPPYFD---YWGQGTTVTV 394
QY 116 SS 117
Db 395 SS 396

RESULT 9
US-09-364-088-16
; Sequence 16, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-16

Query Match 80.4%; Score 507.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 2.8e-43;
Matches 98; Conservative 5; Mismatches 10; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNIKDFYMHVWKORPEQGLEWIGWIDPENGDSGYA 61
Db 278 IKLQSGAELVRSGETSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDT EYA 337
QY 62 PKFGKATMTADSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
Db 338 PKFGKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPGPPYFD---YWGQGTTVTV 394
QY 116 SS 117
Db 395 SS 396

RESULT 10
US-09-102-716-16
; Sequence 16, Application US/09102716

; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 80.4%; Score 507.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 2.8e-43;
Matches 98; Conservative 5; Mismatches 10; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNIKDFYMHVWKORPEQGLEWIGWIDPENGDSGYA 61
Db 278 IKLQSGAELVRSGETSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDT EYA 337
QY 62 PKFGKATMTADSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
Db 338 PKFGKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPGPPYFD---YWGQGTTVTV 394
QY 116 SS 117
Db 395 SS 396

RESULT 11
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-017-57024

Query Match	79.6%	Score 502.5;	DB 1;	Length 124;
Best Local Similarity	76.4%;	Pred. No. 1.5e-43;		
Matches 97;	Conservative	8;	Mismatches 9;	Indels 13;
				Gaps 2;

Qy	1	QVKEQQSGAELVGSGASVKLSCTTSGFNKIDFYMHVYKQRPEQGLEWIGWIDPENGDSGY	60
Dd		: : : :	
Dd	1	EVOEQSGAELVRSGASVKMSCTASGFNIKDYMHVYKQRPEQGLEWIGWIDPENGDTEY	60
Qy	61	APKEQCKATMTADSSNTAYLQLSSLTSED ⁺ TAVYYCNA-----YYGDEYEGYWQG	110
Dd		: :	
Dd	61	APKEQCKATMTDTSSNTAYLQLSSLTSED ⁺ TAVYYCNTRGLSTMITRWFDD---VWGAG	117
Qy	111	TTVAIVSS	117
Dd			
Dd	118	TTVAIVSS	124

RESULT 12
 US-08-471-426-4
 ; Sequence 4 Application US/08471426
 ; Patent No. 5808033
 ; GENERAL INFORMATION:
 ; APPLICANT: GOURLIE, BRIAN B
 ; APPLICANT: RIXON, MARK W
 ; APPLICANT: MEZES, PETER S
 ; APPLICANT: KAPLAN, DONALD A
 ; APPLICANT: SCHLOM, JEFFREY
 ; TITLE OF INVENTION: A NOVEL ANTIGEN CHIMERIC ANTIBODIES
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Duane C. Ulmer
 ; STREET: P.O. Box 1967
 ; CITY: Midland
 ; STATE: MI
 ; COUNTRY: US
 ; ZIP: 48641-1967
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4

Query Match          79.6%; Score 502.5; DB 1; Length 124;
Best Local Similarity 76.4%; Pred. No. 1.5e-43;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;

QY   1 QVKLQQSGAELVCGSASVKLSCTTSGFNKDFYMHVVKQRPEQGLEWIGWIDPENGDSGY 60
      :|:||||||| |||||:|| | |||||:||||| ||||| ||||| ||||| |||||: |
Db    1 EVQLQQSGAELVRGSASVKMSCTASGFNIKDYIMHWVKRPEQGLEWIGWIDPENGDTEY 60

QY   61 APKFQKGATMPADSSNTAYLQLSSLTSEDNAVYYCNA-----YYGDYEGYWGG 110
      ||||| ||||| |:||||| ||||| ||||| ||||| ||||| ||||| ||||| ::| |||
Db    61 APKFQKGATMTDTSNTAYLQLSSLTSEDNAVYYCNTRGSLSTMITTRWFFD---VMGAG 117

QY   111 TTVTVSS 117
      ||| |||
Db    118 TTAVASS 124

RESULT 13
PCT-US94-01709-4
; Sequence 4, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```


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; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

Query Match          100.0%; Score 631; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
Db 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
QY 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||
Db 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||

RESULT 3
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match          100.0%; Score 631; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.1e-41;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
Db 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
QY 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||
Db 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||

RESULT 4
US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
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; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match          100.0%; Score 631; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.1e-41;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
Db 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
QY 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||
Db 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||

RESULT 5
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match          98.9%; Score 624; DB 10; Length 117;
Best Local Similarity 99.1%; Pred. No. 2.1e-41;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
Db 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
    |||||
QY 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||
Db 61 APKFOGKATMTADSSNTAYLQLSLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
    |||||

RESULT 6
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
```


; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,051
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-051-1

Query Match 79.2%; Score 499.5; DB 9; Length 124;
Best Local Similarity 76.4%; Pred. No. 6.2e-32;
Matches 97; Conservative 7; Mismatches 10; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIGWIDPENGDSGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 EVQLQSGAELVSRGASVKLSCTASGFNIDYMHVWKQRPEQGLEWIGWIDPENGDT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YYGDEGYWGQG 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 APKFGKATMTDYSSNTAYLQLSLTSEDYAVYYCNRGLSTMTTRWFFD---VWGAG 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 111 TTVTVSS 117
:|||||:|
Db 118 TTVAVSS 124
:|||||:|

RESULT 11
US-09-910-059-11
; Sequence 11, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-11

Query Match 79.0%; Score 498.5; DB 10; Length 120;
Best Local Similarity 80.8%; Pred. No. 7.2e-32;
Matches 97; Conservative 7; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIGWIDPENGDSGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 EVQLQSGAELVSRGASVKLSCTASGFNIDYMHVWKQRPEQGLEWIAWIDPENGDT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-YYGDY--EGYWGQGTTVTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 APKFRGKATLTADSSNTAYLHLSLTSEDYAVYYCHVLIYAGYLAIDYWGQGTSAVAVSS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 12
US-09-910-059-19
; Sequence 19, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric HuIgG2 Fd construct
US-09-910-059-19

Query Match 79.0%; Score 498.5; DB 10; Length 255;
Best Local Similarity 80.8%; Pred. No. 1.4e-31;
Matches 97; Conservative 7; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 20 EVQLQSGAELVSRGASVKLSCTASGFNIDYMHVWKQRPEQGLEWIAWIDPENGDT 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-YYGDY--EGYWGQGTTVTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 80 APKFRGKATLTADSSNTAYLHLSLTSEDYAVYYCHVLIYAGYLAIDYWGQGTSAVAVSS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 13
US-09-564-329A-11
; Sequence 11, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-11

Query Match 76.8%; Score 484.5; DB 10; Length 136;
Best Local Similarity 77.8%; Pred. No. 9.3e-31;
Matches 91; Conservative 9; Mismatches 12; Indels 5; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db 14 EVQLQSGAELVRSASVKLSCTASGFNIKDYIHWVNQRDPDQGLEWIGWIDPENGDTF 73
QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVSS 117
Db 74 VPKFQKATMTADIFSNYALHLSLTSEDYAVYYCKT-----GGFWGQGTITVSA 125

RESULT 14
US-09-855-153-11
; Sequence 11, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-11

Query Match 76.8%; Score 484.5; DB 10; Length 136;
Best Local Similarity 77.8%; Pred. No. 9.3e-31;
Matches 91; Conservative 9; Mismatches 12; Indels 5; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db 14 EVQLQSGAELVRSASVKLSCTASGFNIKDYIHWVNQRDPDQGLEWIGWIDPENGDTF 73
QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVSS 117
Db 74 VPKFQKATMTADIFSNYALHLSLTSEDYAVYYCKT-----GGFWGQGTITVSA 125

RESULT 15
US-09-854-811-11
; Sequence 11, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-11

Query Match 76.8%; Score 484.5; DB 10; Length 136;
Best Local Similarity 77.8%; Pred. No. 9.3e-31;
Matches 91; Conservative 9; Mismatches 12; Indels 5; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db 14 EVQLQSGAELVRSASVKLSCTASGFNIKDYIHWVNQRDPDQGLEWIGWIDPENGDTF 73
QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVSS 117
Db 74 VPKFQKATMTADIFSNYALHLSLTSEDYAVYYCKT-----GGFWGQGTITVSA 125

Search completed: December 23, 2002, 07:58:19
Job time : 10.8837 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
OM protein - protein search, using sw model
Run on: December 23, 2002, 07:17:57 ; Search time 23.1279 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-7
Perfect score: 631
Sequence: 1 QVKLQSGAELVSGASVKL.....AYYGDYEGYWGQGTTVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	80.7	136	2 S04576	Ig heavy chain pre
2	497.5	78.8	268	2 A56446	Ig heavy chain V r
3	494.5	78.4	116	2 S15672	Ig heavy chain V r
4	487	77.2	118	2 S25174	Ig heavy chain V r
5	481.5	76.3	137	2 S52445	Ig heavy chain V r
6	479	75.9	117	2 S17586	Ig heavy chain V r
7	478	75.8	221	2 S49220	Ig gamma-1 chain -
8	475	75.3	120	2 S03471	Ig heavy chain V-D
9	469.5	74.4	178	2 S29594	Ig gamma chain (WM
10	466	73.9	116	2 S24289	Ig gamma chain V r
11	464.5	73.6	114	4 A47271	nitrophenyl phosph
12	460.5	73.0	122	2 S06823	Ig heavy chain V r
13	454	71.9	120	2 S03484	Ig heavy chain V-D
14	453	71.8	115	2 S03482	Ig heavy chain V-D
15	452	71.6	233	2 JC5322	p53 specific singl
16	434	68.8	108	2 PH1012	Ig heavy chain V r
17	432	68.5	249	2 S41374	single chain Fv an
18	429.5	68.1	115	2 PL0246	Ig heavy chain V r
19	429	68.0	123	2 PH1403	Ig heavy chain V r
20	424.5	67.3	107	2 PH1013	Ig heavy chain V r
21	419.5	66.5	118	2 G37267	Ig heavy chain V r
22	412.5	65.4	139	2 PS0024	Ig heavy chain pre
23	409.5	64.9	115	2 A54378	Ig heavy chain V r
24	409	64.8	138	2 S21810	Ig heavy chain V r
25	405.5	64.3	120	2 B22769	Ig heavy chain V r
26	405	64.2	246	2 S38950	Ig gamma chain - m
27	405	64.2	446	2 S40295	Ig gamma-2a chain
28	403.5	63.9	107	2 A27646	Ig heavy chain V r
29	402.5	63.8	116	2 S53751	antibody Fab Jel 1

ALIGNMENTS

RESULT 1

S04576

Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000

C:Accession: S04576

R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.,

Eur. J. Immunol. 17, 91-95, 1987

A:Title: Molecular analysis of the murine lupus-associated anti-self response: invol

A:Reference number: S04573; MUID:87133856; PMID:3102255

A:Accession: S04576

A:Molecule type: mRNA

A:Residues: 1-136 <KOF>

A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Result

No.	Score	Query Match	Length	DB ID	Description
1	509	80.7	136	2 S04576	Ig heavy chain pre
2	497.5	78.8	268	2 A56446	Ig heavy chain V r
3	494.5	78.4	116	2 S15672	Ig heavy chain V r
4	487	77.2	118	2 S25174	Ig heavy chain V r
5	481.5	76.3	137	2 S52445	Ig heavy chain V r
6	479	75.9	117	2 S17586	Ig heavy chain V r
7	478	75.8	221	2 S49220	Ig gamma-1 chain -
8	475	75.3	120	2 S03471	Ig heavy chain V-D
9	469.5	74.4	178	2 S29594	Ig gamma chain (WM
10	466	73.9	116	2 S24289	Ig gamma chain V r
11	464.5	73.6	114	4 A47271	nitrophenyl phosph
12	460.5	73.0	122	2 S06823	Ig heavy chain V r
13	454	71.9	120	2 S03484	Ig heavy chain V-D
14	453	71.8	115	2 S03482	Ig heavy chain V-D
15	452	71.6	233	2 JC5322	p53 specific singl
16	434	68.8	108	2 PH1012	Ig heavy chain V r
17	432	68.5	249	2 S41374	single chain Fv an
18	429.5	68.1	115	2 PL0246	Ig heavy chain V r
19	429	68.0	123	2 PH1403	Ig heavy chain V r
20	424.5	67.3	107	2 PH1013	Ig heavy chain V r
21	419.5	66.5	118	2 G37267	Ig heavy chain V r
22	412.5	65.4	139	2 PS0024	Ig heavy chain pre
23	409.5	64.9	115	2 A54378	Ig heavy chain V r
24	409	64.8	138	2 S21810	Ig heavy chain V r
25	405.5	64.3	120	2 B22769	Ig heavy chain V r
26	405	64.2	246	2 S38950	Ig gamma chain - m
27	405	64.2	446	2 S40295	Ig gamma-2a chain
28	403.5	63.9	107	2 A27646	Ig heavy chain V r
29	402.5	63.8	116	2 S53751	antibody Fab Jel 1

Query Match 80.7%; Score 509; DB 2; Length 136;

Best Local Similarity 82.9%; Pred. No. 1.4e-38;

Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPENGDSGY 60

:|:||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |

Db 20 EVQLQSGAELVRPGASVKLSCTASGFNKKIDYMHVVKQRPEQGLEWIGWIDPENGDTQY 79

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTTVTVSS 117

| |||||||||:|||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 80 ASKFGKATMTADTSSNTYTLQLSSLTSEDYAVYCTTYGAYAMDYWGQGTSTVTVSS 136

RESULT 2

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally id.

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 78.8%; Score 497.5; DB 2; Length 268;

Best Local Similarity 83.1%; Pred. No. 3e-37;

R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 71.6%; Score 452; DB 2; Length 233;
Best Local Similarity 79.6%; Pred. No. 3e-33;
Matches 90; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

QY 5 QQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSGYAPKF 64
|:||||| ||||| ||||| ||||| |:|||||:||||| ||||| |||||:
Db 1 QESGAELVRSGASVKLSCTTSGFNINDYYMHVWKRRPEQGLEWIGRIDPENGADMTRSS 60

QY 65 QGKATMTADSSNTAYLQLSLSLTSEDYVYYCNAYYGDYEGYWGQGTTVTSS 117
|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GVKATMTADTSSNTAYLQLSLSLTSEDYVYYCNAGM----DYWGQGTTVTSS 109

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Job time : 24.1279 secs

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GenCore version 5.1.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 11.564 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-7
Perfect score: 631
Sequence: 1 QVKLQQSGAELVGSASVKL.....AYYGDYEGYWGQGTVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	402.5	63.8	139	1	HV07_MOUSE	P01751 mus musculus
2	389	61.6	120	1	HV03_MOUSE	P01747 mus musculus
3	384.5	60.9	137	1	HV11_MOUSE	P01755 mus musculus
4	380	60.2	140	1	HV02_MOUSE	P01746 mus musculus
5	377	59.7	117	1	HV12_MOUSE	P01756 mus musculus
6	373	59.1	138	1	HV48_MOUSE	P03980 mus musculus
7	368	58.3	117	1	HV13_MOUSE	P01757 mus musculus
8	368	58.3	136	1	HV15_MOUSE	P01759 mus musculus
9	365.5	57.9	120	1	HV50_MOUSE	P06329 mus musculus
10	363.5	57.6	147	1	HV1C_HUMAN	P01744 homo sapien
11	362.5	57.4	118	1	HV51_MOUSE	P06330 mus musculus
12	347	55.0	121	1	HV01_MOUSE	P01745 mus musculus
13	344	54.5	117	1	HV06_MOUSE	P01750 mus musculus
14	342	54.2	117	1	HV09_MOUSE	P01753 mus musculus
15	338	53.6	117	1	HV04_MOUSE	P01748 mus musculus
16	335	53.1	117	1	HV49_MOUSE	P06328 mus musculus
17	331	52.5	117	1	HV10_MOUSE	P01754 mus musculus
18	331	52.5	117	1	HV52_MOUSE	P06327 mus musculus
19	327	51.8	117	1	HV14_MOUSE	P01758 mus musculus
20	327	51.8	117	1	HV1B_HUMAN	P01743 homo sapien
21	324	51.3	117	1	HV05_MOUSE	P01749 mus musculus
22	322.5	51.1	119	1	HV40_MOUSE	P01810 mus musculus
23	320.5	50.8	119	1	HV37_MOUSE	P01807 mus musculus
24	315.5	50.0	114	1	HV00_MOUSE	P01741 mus musculus
25	313.5	49.7	119	1	HV38_MOUSE	P01808 mus musculus
26	311	49.3	117	1	HV42_MOUSE	P01812 mus musculus
27	308	48.8	117	1	HV1G_HUMAN	P23083 homo sapien
28	307.5	48.7	122	1	HV3G_HUMAN	P01768 homo sapien
29	307.5	48.7	136	1	HV16_MOUSE	P01783 mus musculus
30	305	48.3	142	1	HV01_RAT	P01805 rattus norv
31	302	47.9	117	1	HV1A_HUMAN	P01742 homo sapien
32	295	46.8	118	1	HV39_MOUSE	P01809 mus musculus
33	292	46.3	117	1	HV41_MOUSE	P01811 mus musculus

34	289.5	45.9	122	1	HV21_MOUSE	P01790 mus musculus
35	289	45.8	113	1	HV30_MOUSE	P01799 mus musculus
36	289	45.8	115	1	HV32_MOUSE	P01801 mus musculus
37	289	45.8	119	1	HV3L_HUMAN	P01773 homo sapien
38	289	45.8	125	1	HV1F_HUMAN	P06326 homo sapien
39	287	45.5	123	1	HV24_MOUSE	P01793 mus musculus
40	285	45.2	113	1	HV31_MOUSE	P01800 mus musculus
41	284	45.0	113	1	HV27_MOUSE	P01796 mus musculus
42	283.5	44.9	122	1	HV3A_HUMAN	P01762 homo sapien
43	283	44.8	115	1	HV33_MOUSE	P01802 mus musculus
44	283	44.8	123	1	HV19_MOUSE	P01788 mus musculus
45	281.5	44.6	116	1	HV3T_HUMAN	P01781 homo sapien

ALIGNMENTS

RESULT 1
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 63.8%; Score 402.5; DB 1; Length 139;
Best Local Similarity 65.8%; Pred. No. 2.1e-33;

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DR	EMBL; J00493; AAA38128.1; -.
DR	PIR; A02028; HVMSG7.
DR	HSSP; P01810; 2FEJ.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin v region; Antiarsonate antibody; Hybridoma; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT	NON_TER 140 140
SO	SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26342; MHMSJ5.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 58.3%; Score 368; DB 1; Length 117;
Best Local Similarity 61.3%; Pred. No. 4.7e-30;
Matches 73; Conservative 16; Mismatches 26; Indels 4; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db :||||| ||| |||||:| ||: |:|| |||| : |||| |:|| :|
1 EVQLQSGPELVKPGASVKMSCKASGYFTDYMKWKVQSHGKSLEWIGDINPNNGTSY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYVC--NAYYGDYEGYWGQTTVTYSS 117
Db ||:||||:| ||:||||:|||||||:|||| :|: | |||||
61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYW--YFDVWGAGTTVTYSS 117

RESULT 8
HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -----
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CC -----
DR EMBL; J00494; AAA38130.1; -.
DR PIR; A02042; HVMSB1.
DR HSSP; P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 58.3%; Score 368; DB 1; Length 136;
Best Local Similarity 59.0%; Pred. No. 5.6e-30;
Matches 69; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db ||:|||| |:|| ||||| ||: |:||||| : |||| | ||:|
20 QVQLQSGPEVVRPGVSVKISCKSGYFTTDYAMHWVKQSHAKSLEWIGVISYNGNTSY 79

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQTTVTYSS 117
Db ||:|||| |:|| :||: ||||| || ||||| |||||:||||
80 NQKFKGKATMTVDKSSSTVHMLARLTSEDSANLYCARYYGNFYDYWGQGTTLTYSS 136

RESULT 9
HV50_MOUSE STANDARD; PRT; 120 AA.
ID HV50_MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 57.9%; Score 365.5; DB 1; Length 120;
Best Local Similarity 58.2%; Pred. No. 8.6e-30;
Matches 71; Conservative 15; Mismatches 29; Indels 7; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db ||:| | ||| |||| | ||: :|||: || ||||| |:|| |:
1 QVQLQPGTELVKPGASVNLCKASGYTFTSYMHWIRQRPQGQGLEWIGGINPGGTNY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEG-----YWGQTTVTY 115
Db ||: |||: | ||: | |||: |||||: |||| : |||| | |||||
61 NEKFKSKATLTVDKSSSATYMQLSLTPTSEDSAVYYCARW--DYEGDRYFDVWGTTVTY 118

QY 116 SS 117
Db ||
119 SS 120


```
DR PIR; A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 53.6%; Score 338; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 4.6e-27;
Matches 64; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNICKDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
Db 20 QVQLQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGLEWIGNINPGNGGTNY 79

QY 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYIC 96
Db 80 NEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYIC 115
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Job time : 12.564 secs

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QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYC--NAYYGDYEGYWGQGTTVTVSS 117
IIIIII III:III:IIIIIIIIIIIIIIIIIIII III I II I IIIIIII:IIII
Db 80 APKFGKATITADTSSNTAYLQLSSLTSEDYAVYYCARNLLYGGYDYWGQGTITVSS 138

RESULT 2
Q9JL85
ID Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 67.7%; Score 427; DB 11; Length 109;
Best Local Similarity 77.1%; Pred. No. 2e-35;
Matches 84; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 9 AEIVGSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGYAPKFQGA 68
IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII III I I IIIIIII
Db 1 AEIVKPGASVKLSCTASGFNIEDTYMHVWKQRPQGLEWIGRIDPATGHSKYDPKFQGA 60

QY 69 TMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTTVTVSS 117
IIII III:III:IIIIIIIIIIIIIIIIIIII IIIIIII:IIII
Db 61 TMTDSSNTAYLQLSSLTSEDYAVYYCVRGAVVFDYWGQGTALTVSS 109

RESULT 3
Q924P9
ID Q924P9 PRELIMINARY; PRT; 143 AA.
AC Q924P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
GN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069916; BAB63932.1; -.
DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match 65.1%; Score 410.5; DB 11; Length 143;
Best Local Similarity 66.9%; Pred. No. 1.3e-33;
Matches 79; Conservative 14; Mismatches 24; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
II:III IIIII IIIIIIIII II: :I IIIII IIII :I
Db 1 QVQLQQLGAELVKPGASVKLSCKASGYTFTSYMQWVKQRPQGQLEWIGEIDPSDYTNY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYC-NAYYGDYEGYWGQGTTVTVSS 117
II:III:II:III:IIIIIIIIIIIIIIIIII:III:III IIIII:IIII
Db 61 NQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYYCASHYYGSSSDYWGQGTTLTVSS 118

RESULT 4
Q924R8
ID Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match 64.3%; Score 406; DB 11; Length 146;
Best Local Similarity 65.3%; Pred. No. 3.6e-33;
Matches 79; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
II:III IIIII IIIIIIIII II: :IIIIII IIIII:IIII III:II
Db 1 QVQLQPGAELVKPGASVKLSCKASGYTFTSYMHVWKQRPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYC-NAYYGD---YEGYWGQGTTVTVS 116
II: III:II:III:IIIIIIIIIIIIIIIIII:IIII:III I IIIII:IIII
Db 61 NEKFKKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSYYGSSLYFDYWGQGTTLTVS 120

QY 117 S 117
Db 121 S 121

RESULT 5
Q924Q7
ID Q924Q7 PRELIMINARY; PRT; 145 AA.
AC Q924Q7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB067795; BAB63280.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match 63.0%; Score 397.5; DB 11; Length 143;
Best Local Similarity 65.5%; Pred. No. 2.5e-32;
Matches 78; Conservative 14; Mismatches 24; Indels 3; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
||:|||| ||||| ||||| ||: ||||| ||: ||||| ||: ||: |
Db 1 QVQLQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKORPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGY--WGQGTVTVTVSS 117
||: ||||: | | ||||: ||||| ||||| : ||||: || ||||| ||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARFY-DYEYFDVWGTTVTVTVSS 118

RESULT 12
Q924R2
ID Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB067788; BAB63273.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 1
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 62.9%; Score 397; DB 11; Length 140;
Best Local Similarity 66.1%; Pred. NO. 2.8e-32;
Matches 78; Conservative 13; Mismatches 23; Indels 4; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
||:|||| ||||| ||||| ||: ||||| ||: ||||| ||: ||: |
Db 1 QVQLQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKORPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVTVSS 117
||: ||||: | | ||||: ||||| ||||| | || ||||| |||||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYICARIYAGD---YWGQGTSVTVSS 115

RESULT 13
Q924Q1
ID Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB069913; BAB63929.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 1
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 62.8%; Score 396; DB 11; Length 142;
Best Local Similarity 65.0%; Pred. No. 3.5e-32;
Matches 76; Conservative 13; Mismatches 28; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
||:|||| | ||| ||||| ||: ||: ||||| ||||| ||: ||: |
Db 1 QVQLQPGTELKPGASVKLSCKASGYTFTSYWMHWVKORPQGQGLEWIGNPNSGGTNY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVTVSS 117
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Db 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGWEAMDYWGQGTSVTVSS 117

RESULT 14
Q924R4
ID Q924R4 PRELIMINARY; PRT; 145 AA.
AC Q924R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB067785; BAB63270.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16081 MW; ECDB1A135E05B8AA CRC64;

Query Match 62.5%; Score 394.5; DB 11; Length 145;
Best Local Similarity 64.2%; Pred. No. 5.1e-32;
Matches 77; Conservative 14; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
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Db 1 QVQLQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKORPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYE---GYWGQGTVTVTVSS 117
||: ||||: | | ||||: ||||| ||||| ||: ||||| |||||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSDYDYDYAMDYWGQGTSVTVSS 120

RESULT 15
Q924R1
ID Q924R1 PRELIMINARY; PRT; 145 AA.

Search completed: December 23, 2002, 07:29:55
Job time : 49:5233 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 19.4651 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIELTQSPAIMSASPGEKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext.0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	541	97.0	108	4 US-09-171-945-9	Sequence 9, Appl1
2	539	96.6	235	4 US-09-171-945-17	Sequence 17, Appl1
3	534	95.7	129	2 US-08-116-778E-2	Sequence 2, Appl1
4	534	95.7	129	2 US-08-438-562-2	Sequence 2, Appl1
5	534	95.7	129	2 US-08-483-528B-92	Sequence 92, Appl1
6	532	95.3	270	2 US-08-652-507-2	Sequence 2, Appl1
7	532	95.3	553	2 US-08-661-052-16	Sequence 16, Appl1
8	532	95.3	553	4 US-09-188-082-16	Sequence 16, Appl1
9	532	95.3	553	4 US-09-364-088-16	Sequence 16, Appl1
10	532	95.3	553	4 US-09-102-716-16	Sequence 16, Appl1
11	526	94.3	281	4 US-09-423-439-44	Sequence 44, Appl1
12	526	94.3	666	4 US-09-423-439-51	Sequence 51, Appl1
13	518	92.8	105	3 US-08-434-000A-12	Sequence 12, Appl1
14	518	92.8	105	4 US-09-312-157-12	Sequence 12, Appl1
15	516	92.5	106	1 US-07-634-278-1	Sequence 1, Appl1
16	516	92.5	106	1 US-07-634-278-16	Sequence 16, Appl1
17	516	92.5	106	1 US-08-477-728-1	Sequence 1, Appl1
18	516	92.5	106	1 US-08-477-728-16	Sequence 16, Appl1
19	516	92.5	106	1 US-08-474-040-1	Sequence 1, Appl1
20	516	92.5	106	1 US-08-474-040-16	Sequence 16, Appl1
21	516	92.5	106	1 US-08-487-200-1	Sequence 1, Appl1
22	516	92.5	106	1 US-08-487-200-16	Sequence 16, Appl1
23	516	92.5	106	1 US-08-488-113B-163	Sequence 163, App
24	516	92.5	106	1 US-08-477-484B-163	Sequence 163, App
25	516	92.5	106	1 US-08-107-669D-49	Sequence 49, Appl1
26	516	92.5	106	1 US-08-472-788A-83	Sequence 83, Appl1
27	516	92.5	106	2 US-08-477-531B-49	Sequence 49, Appl1

28	516	92.5	106	2 US-08-646-360-163	Sequence 163, App
29	516	92.5	106	2 US-08-082-842A-83	Sequence 83, Appl1
30	516	92.5	106	4 US-08-839-765-163	Sequence 163, App
31	516	92.5	106	4 US-09-136-389-163	Sequence 163, App
32	516	92.5	106	4 US-08-484-537-1	Sequence 1, Appl1
33	516	92.5	106	4 US-08-484-537-16	Sequence 16, Appl1
34	516	92.5	106	4 US-09-610-838-163	Sequence 163, App
35	516	92.5	239	3 US-08-279-772A-8	Sequence 8, Appl1
36	516	92.5	239	4 US-08-902-486-11	Sequence 11, Appl1
37	516	92.5	599	1 US-08-463-163-3	Sequence 3, Appl1
38	498	89.2	130	4 US-09-393-385B-113	Sequence 113, App
39	495	88.7	130	4 US-09-393-385B-111	Sequence 111, App
40	490	87.8	246	1 US-08-469-486-57	Sequence 57, Appl1
41	490	87.8	246	2 US-08-469-658-57	Sequence 57, Appl1
42	489	87.6	128	4 US-08-619-491-2	Sequence 2, Appl1
43	489	87.6	128	5 PCT-US95-07302-2	Sequence 2, Appl1
44	486	87.1	107	1 US-08-211-202-3	Sequence 3, Appl1
45	483	86.6	244	2 US-08-553-497A-20	Sequence 20, Appl1

ALIGNMENTS

RESULT 1
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match	97.0%;	Score 541;	DB 4;	Length 108;
Best Local Similarity	95.4%;	Pred. No. 1.4e-41;		
Matches 103;	Conservative 4;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60			
Db 1	DIELTQSPAIMSASPGEKVTITCSASSSVTYMHWFQKPGTSPKLIYSTSNLASGVPAR 60			
Qy 61	FSGSGGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIKRA 108			
Db 61	FSGSGGTSYSLTISRMEADAATYTCQORSTYPLTFGAGTKLEIKRA 108			

RESULT 2
US-09-171-945-17
; Sequence 17, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek


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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-16

Query Match          95.3%; Score 532; DB 4; Length 553;
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPARFSG 63
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Db 415 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPARFSG 474

QY 64 SSGTSSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
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Db 475 SSGTSSYSLTISRMEADAATYYCQQRSSYPLTFGAGTKLELKRA 519

RESULT 9
US-09-364-088-16
; Sequence 16, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-16

Query Match          95.3%; Score 532; DB 4; Length 553;
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPARFSG 63
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 415 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPARFSG 474

QY 64 SSGTSSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
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Db 475 SSGTSSYSLTISRMEADAATYYCQQRSSYPLTFGAGTKLELKRA 519
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RESULT 10
US-09-102-716-16
; Sequence 16, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match          95.3%; Score 532; DB 4; Length 553;
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPARFSG 63
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QY 64 SSGTSSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
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Db 475 SSGTSSYSLTISRMEADAATYYCQQRSSYPLTFGAGTKLELKRA 519

RESULT 11
US-09-423-439-44
; Sequence 44, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
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Best Local Similarity 93.3%; Pred. No. 1.6e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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RESULT 14

US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-351
; SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Guy's 13 Kappa
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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Best Local Similarity 93.3%; Pred. No. 1.6e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 DIVMTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 105
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Db 61 FSGSGSGTSYSLTISRMEADAATYYCHQRTSYPTYTFGGGTKLEI 105

RESULT 15

US-07-634-278-1
; Sequence 1, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..106
; OTHER INFORMATION: /note= "Variable region of the mouse
; OTHER INFORMATION: anti-Tac antibody light chain."
US-07-634-278-1

Query Match 92.5%; Score 516; DB 1; Length 106;
Best Local Similarity 93.3%; Pred. No. 2.4e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 10.0465 Seconds
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Title: US-09-865-198-8
Perfect score: 558
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	558	100.0	108	10	US-09-865-198-8 Sequence 8, Appli
3	558	100.0	240	10	US-09-976-787-28 Sequence 28, Appl
4	558	100.0	240	10	US-09-865-198-27 Sequence 27, Appl
5	549	98.4	106	10	US-09-976-787-24 Sequence 24, Appl
6	549	98.4	106	10	US-09-865-198-23 Sequence 23, Appl
7	549	98.4	238	10	US-09-976-787-29 Sequence 29, Appl
8	549	98.4	238	10	US-09-865-198-28 Sequence 28, Appl
9	541	97.0	108	10	US-09-910-059-9 Sequence 9, Appli
10	539	96.6	235	10	US-09-910-059-17 Sequence 17, Appl
11	523	93.7	669	9	US-09-807-721-2 Sequence 2, Appli
12	518	92.8	105	9	US-09-982-107-12 Sequence 12, Appl
13	509	91.2	107	9	US-09-144-886-88 Sequence 88, Appl
14	506	90.7	119	10	US-09-808-037-28 Sequence 28, Appl
15	506	90.7	239	10	US-09-808-037-6 Sequence 6, Appli
16	505	90.5	107	9	US-09-144-886-76 Sequence 76, Appl
17	500	89.6	107	9	US-09-144-886-90 Sequence 90, Appl
18	489	87.6	107	9	US-09-144-886-75 Sequence 75, Appl
19	489	87.6	107	9	US-09-144-886-78 Sequence 78, Appl

20	484	86.7	107	9	US-09-144-886-82	Sequence 82, Appl
21	484	86.7	107	9	US-09-144-886-83	Sequence 83, Appl
22	484	86.7	109	9	US-09-144-886-91	Sequence 91, Appl
23	483	86.6	131	10	US-09-881-823-6	Sequence 6, Appli
24	479.5	85.9	112	9	US-09-144-886-89	Sequence 89, Appl
25	471	84.4	109	9	US-09-144-886-96	Sequence 96, Appl
26	466	83.5	107	10	US-09-965-099-11	Sequence 11, Appl
27	466	83.5	107	12	US-10-051-852-11	Sequence 11, Appl
28	466	83.5	109	9	US-09-144-886-79	Sequence 79, Appl
29	466	83.5	112	10	US-09-965-099-103	Sequence 103, App
30	466	83.5	112	12	US-10-051-852-103	Sequence 103, App
31	465	83.3	109	9	US-09-144-886-97	Sequence 97, Appl
32	463	83.0	106	10	US-09-158-120A-35	Sequence 35, Appl
33	461	82.6	106	10	US-09-965-099-105	Sequence 105, App
34	461	82.6	106	12	US-10-051-852-105	Sequence 105, App
35	459	82.3	109	9	US-09-144-886-77	Sequence 77, Appl
36	459	82.3	109	9	US-09-144-886-98	Sequence 98, Appl
37	458	82.1	107	10	US-09-910-059-71	Sequence 71, Appl
38	458	82.1	235	10	US-09-910-059-99	Sequence 99, Appl
39	449	80.5	127	10	US-09-753-436-80	Sequence 80, Appl
40	448	80.3	106	10	US-09-893-615-89	Sequence 89, Appl
41	447	80.1	107	10	US-09-910-059-61	Sequence 61, Appl
42	445	79.7	107	10	US-09-910-059-50	Sequence 50, Appl
43	445	79.7	235	10	US-09-910-059-52	Sequence 52, Appl
44	442	79.2	109	9	US-09-144-886-92	Sequence 92, Appl
45	437	78.3	107	10	US-09-910-059-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-976-787-8

; Sequence 8, Application US/09976787

; Patent No. US20020064528A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; APPLICANT: Witte, Larry

; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

; FILE REFERENCE: 11245/46505

; CURRENT APPLICATION NUMBER: US/09/976,787

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/493,539

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 8

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-976-787-8

Query Match	100.0%;	Score 558;	DB 10;	Length 108;
Best Local Similarity	100.0%;	Pred. No. 1.7e-31;		
Matches	108;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIYSTNLSASGVPAR	60	
Db	1	DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIYSTNLSASGVPAR	60	
Qy	61	FSGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA	108	
Db	61	FSGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA	108	

RESULT 2

US-09-865-198-8

; Sequence 8, Application US/09865198

; Patent No. US20020103345A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping


```

; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match          100.0%; Score 558; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
   |||
Db 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
   |||
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
   |||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
   |||

RESULT 3
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match          100.0%; Score 558; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.1e-31;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
   |||
Db 133 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 192
   |||
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
   |||
Db 193 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 240
   |||

RESULT 4
US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
```

```

; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match          100.0%; Score 558; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.1e-31;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
   |||
Db 133 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 192
   |||
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
   |||
Db 193 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 240
   |||

RESULT 5
US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match          98.4%; Score 549; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
   |||
Db 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
   |||
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
   |||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
   |||

RESULT 6
US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
```

```

; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

```

Query Match	98.4%;	Score 549;	DB 10;	Length 106;
Best Local Similarity	100.0%;	Pred. No. 6.7e-31;		
Matches 106;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Qy	61 FSGSGGTSYSLTISRMEADAATYYCQRSSYPFTFGSGTKLEIK 106
D_b	61 FSGSGGTSYSLTISRMEADAATYYCQRSSYPFTFGSGTKLEIK 106

RESULT 7
US-09-976-787-29

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; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Wordperfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

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```
Query Match          98.4%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 DIELTQSPALMSASPGKEKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASYPAR 60
|||
Db 133 DIELTQSPALMSASPGKEKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASYPAR 192

Qy 61 FSGSGGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 106
 |||||
 Db 193 FSGSGGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 238

```

RESULT 8
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglob
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows

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; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

```

Query Match	98.4%;	Score 549;	DB 10;	Length 238;
Best Local Similarity	100.0%;	Pred. No. 1.2e-30;		
Matches 106;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

QY	61	FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK	106
Dp	193	FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK	238

```

RESULT 9
US-09-910-059-9
; Sequence 9, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody t
; TITLE OF INVENTION: Their Therapeutic us
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9

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Query Match 97.0%; Score 541; DB 10; Length 108;
Best Local Similarity 95.4%; Pred. NO. 2.3e-30;
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy	1	DIELTQSPAIMSAPGEKVITCSASSSVYMHWFQKPGTSPKLWIYSTNLASGVPAR	60
		:	:
D_b	1	DIELTQSPAIMSAPGEKVITCSASSVTYMHWFQKPGTSPKLWIYSTNLASGVPAR	60

QY 61 FSGSGTSSLTISRFAEDAATYYCQRRSSYPFTFGSGTKIEKRA 108
|||||

Db 61 FSGSGTSSLTISRFAEDAATYYCQRRSSYPFTFGSGTKIEKRA 108
|||||

RESULT 10
US-09-910-059-17
; Sequence 17, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Anti-
; TITLE OF INVENTION: Their Therapeu
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910

```

; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric light chain sequence
US-09-910-059-17

Query Match          96.6%; Score 539; DB 10; Length 235;
Best Local Similarity 96.3%; Pred. No. 5.6e-30;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 DIELTQSPAIMSASPGKVTITCSASSSVTYMHWFQKPGTSPKLIWYSTSNLASGVPAR 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FSGSGSGTSYSLTISRMEADAATYYCQQRSTYPLTFGAGTKLEIKR 129

RESULT 11
US-09-807-721-2
; Sequence 2, Application US/09807721
; Patent No. US20020174453A1
; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,721
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-721-2

Query Match          93.7%; Score 523; DB 9; Length 669;
Best Local Similarity 92.5%; Pred. No. 1.4e-28;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 457 DIVMTQSPAIMSASPGKVTITCSASSMVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 516
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 517 FSGSGSGTSYSLTISRMEADAATYYCHQRTSYPTYTFGGGKLEIKR 563

RESULT 12
US-09-982-107-12
; Sequence 12, Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIAFT, ANDREW C.
; APPLICANT: HEIN, MICH B.
```

```

; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 kappa
US-09-982-107-12

Query Match          92.8%; Score 518; DB 9; Length 105;
Best Local Similarity 93.3%; Pred. No. 7.7e-29;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FSGSGSGTSYSLTISRMEADAATYYCHQRTSYPTYTFGGGKLEI 105

RESULT 13
US-09-144-886-88
; Sequence 88, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/a clone
US-09-144-886-88

Query Match          91.2%; Score 509; DB 9; Length 107;
Best Local Similarity 97.0%; Pred. No. 3.1e-28;
Matches 97; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSG 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGG 100

RESULT 14
US-09-808-037-28
; Sequence 28, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
```

```

; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 119
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-808-037-28

Query Match          90.7%; Score 506; DB 10; Length 119;
Best Local Similarity 90.6%; Pred. No. 5.3e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR 60
    |||||||||||||||:|||||:||||| ||| || |||||||
Db 14 DIELTQSPAIMASPGKVTITCSASSISYMHWYQQKPGTSPKRWIYDTSKLASGVPAR 73

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
    ||||||||||| ||||||| ||||||| ||||
Db 74 FSGSGSGTSYSLTISSMEADAATYYCHORSSYPFTFGGGAKEIK 119

RESULT 15
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6

Query Match          90.7%; Score 506; DB 10; Length 239;
Best Local Similarity 90.6%; Pred. No. 9e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR 60
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Db 134 DIELTQSPAIMASPGKVTITCSASSISYMHWYQQKPGTSPKRWIYDTSKLASGVPAR 193

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
    ||||||||||| ||||||| ||||||| ||||
Db 194 FSGSGSGTSYSLTISSMEADAATYYCHORSSYPFTFGGGAKEIK 239

Search completed: December 23, 2002, 07:58:20
Job time : 11.0465 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 21.3488 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIELTQSPAIMASPGKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	517	92.7	140	2 PL0013	Ig kappa chain pre
2	513	91.9	106	2 B54378	Ig light chain V r
3	492	88.2	132	2 S05268	Ig kappa chain pre
4	487	87.3	107	2 PC4405	Ig kappa chain V r
5	486	87.1	99	2 D38601	Ig kappa chain V r
6	483	86.6	130	2 A32513	Ig kappa chain pre
7	481	86.2	107	2 A30562	Ig kappa chain V r
8	476	85.3	107	2 B30562	Ig kappa chain V r
9	474	84.9	106	2 G27887	Ig kappa chain V r
10	473	84.8	130	1 JL0079	Ig kappa chain pre
11	472	84.6	106	2 PS0070	Ig kappa chain V r
12	470	84.2	105	2 S26338	Ig kappa chain V r
13	466	83.5	120	2 S66536	Ig light chain V r
14	465	83.3	103	2 S29591	Ig kappa chain V r
15	465	83.3	107	2 PD0011	Ig kappa chain V r
16	465	83.3	108	2 PL0278	Ig kappa chain V r
17	464.5	83.2	108	2 G30560	Ig kappa chain V r
18	463	83.0	106	2 PS0071	Ig kappa chain V r
19	461	82.6	104	2 B49049	Ig kappa chain V r
20	461	82.6	108	2 PL0276	Ig kappa chain V r
21	461	82.6	108	2 PL0277	Ig kappa chain V r
22	460	82.4	235	2 S25058	Ig kappa chain - m
23	458	82.1	91	2 S17626	Ig kappa chain V r
24	455	81.5	107	2 A42848	Ig light chain V r
25	455	81.5	107	2 PT0406	Ig kappa chain V r
26	455	81.5	130	2 B32456	Ig kappa chain pre
27	453	81.2	107	2 S11119	Ig kappa chain V r
28	453	81.2	108	2 PS0069	Ig kappa chain V r
29	453	81.2	123	2 S05269	Ig kappa chain pre

30	451.5	80.9	108	2 S38720	Ig light chain V r
31	451	80.8	107	2 S11118	Ig kappa chain V r
32	450	80.6	91	2 S17630	Ig kappa chain V r
33	450	80.6	104	2 JC6076	anti-D-dimer monoc
34	448	80.3	107	2 PT0401	Ig light chain V r
35	448	80.3	120	2 A34871	Ig kappa chain V r
36	446	79.9	100	2 S29590	Ig kappa chain V r
37	446	79.9	107	2 PT0398	Ig light chain V r
38	446	79.9	108	2 S29581	Ig kappa chain V r
39	446	79.9	130	2 S04573	Ig kappa chain pre
40	445	79.7	107	2 S11121	Ig kappa chain V r
41	442	79.2	107	2 PT0402	Ig light chain V r
42	441	79.0	106	2 PL0082	Ig kappa chain V r
43	441	79.0	107	2 PT0403	Ig light chain V r
44	440	78.9	97	2 S26341	Ig light chain V r
45	440	78.9	113	2 S03410	Ig kappa chain pre

ALIGNMENTS

RESULT 1

PL0013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C;Accession: PL0013

R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424

A;Accession: PL0013

A;Molecule type: mRNA

A;Residues: 1-140 <CHE>

A;Experimental source: cell line 4C11

C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F;38-111/Domain: immunoglobulin homology <IMM>

F;46-55/Region: complementarity-determining 1

F;71-77/Region: complementarity-determining 2

F;110-118/Region: complementarity-determining 3

F;130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match

Best Local Similarity 92.7%; Score 517; DB 2; Length 140;

Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGYVPARF 61

Db 24 IVLTQSPAIMASPGKVTITCSASSSVSYMHWFQQKPDTPKLIYSTSNLASGYVPVRF 83

QY 62 SGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108

Db 84 SGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEMKRA 130

RESULT 2

B54378

Ig light chain V region anti-triplex DNA - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: B54378

R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluor

A;Reference number: A54378; MUID:94165109; PMID:7509814

A;Accession: B54378

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <AGA>

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C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000
C;Accession: PD0011
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from hum
A;Reference number: PC4405
A;Contents: Spleen
A;Accession: PD0011
A;Molecule type: mRNA
A;Residues: 1-107 <DEN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 465; DB 2; Length 107;
Best Local Similarity 85.0%; Pred. No. 5.3e-31;
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPCTSPKLIWYSTSNLASGVPA 60
Db 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPCTSPKLIWYSTSNLASGVPA 60
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
Db 61 GSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKR 107

Search completed: December 23, 2002, 07:31:38
Job time : 21.3488 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 10.6744 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIELTQSPAIMSASPGKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	82.8	107	1 KV6F_MOUSE	P04940 mus musculus
2	457	81.9	107	1 KV6L_MOUSE	P04943 mus musculus
3	457	81.9	107	1 KV6J_MOUSE	P04944 mus musculus
4	456	81.7	107	1 KV6H_MOUSE	P04942 mus musculus
5	455	81.5	107	1 KV6G_MOUSE	P04941 mus musculus
6	450	80.6	108	1 KV6K_MOUSE	P04945 mus musculus
7	433	77.6	107	1 KV6B_MOUSE	P01676 mus musculus
8	430	77.1	107	1 KV6A_MOUSE	P01675 mus musculus
9	429	76.9	107	1 KV6D_MOUSE	P01678 mus musculus
10	428	76.7	107	1 KV6C_MOUSE	P01677 mus musculus
11	413	74.0	107	1 KV6E_MOUSE	P01679 mus musculus
12	410	73.5	129	1 KV4A_MOUSE	P01680 mus musculus
13	373.5	66.9	111	1 KV3M_MOUSE	P01665 mus musculus
14	368.5	66.0	108	1 KV1V_HUMAN	P04430 homo sapien
15	368.5	66.0	111	1 KV3O_MOUSE	P01667 mus musculus
16	366.5	65.7	111	1 KV3L_MOUSE	P01664 mus musculus
17	365.5	65.5	108	1 KV1O_HUMAN	P01607 homo sapien
18	363.5	65.1	111	1 KV3H_MOUSE	P01660 mus musculus
19	362.5	65.0	108	1 KV1B_HUMAN	P01594 homo sapien
20	362.5	65.0	111	1 KV3J_MOUSE	P01662 mus musculus
21	362.5	65.0	111	1 KV3N_MOUSE	P01666 mus musculus
22	361.5	64.8	111	1 KV3Q_MOUSE	P01669 mus musculus
23	361.5	64.8	111	1 KV3S_MOUSE	P01671 mus musculus
24	360.5	64.6	131	1 KV3I_MOUSE	P01661 mus musculus
25	359.5	64.4	111	1 KV3R_MOUSE	P01670 mus musculus
26	358.5	64.2	111	1 KV3K_MOUSE	P01663 mus musculus
27	357.5	64.1	129	1 KV1W_HUMAN	P04431 homo sapien
28	355.5	63.7	108	1 KV5J_MOUSE	P01643 mus musculus
29	354.5	63.5	108	1 KV1H_HUMAN	P01600 homo sapien
30	354.5	63.5	111	1 KV3T_MOUSE	P01672 mus musculus
31	354	63.4	110	1 KV3P_MOUSE	P01668 mus musculus
32	354	63.4	129	1 KV3M_HUMAN	P18136 homo sapien
33	353.5	63.4	108	1 KV1L_HUMAN	P01604 homo sapien

ALIGNMENTS

RESULT 1									
ID	KV6F_MOUSE	STANDARD;	PRT;	107 AA.					
AC	P04940;								
DT	13-AUG-1987 (Rel. 05, Created)								
DT	13-AUG-1987 (Rel. 05, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	Ig kappa chain V-VI region NQ2-17.4.1.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=83271467; PubMed=6877353;								
RA	Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;								
RT	"mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";								
RL	Nature 304:320-324(1983).								
CC	-!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.								
CC	-----								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; K00735; AAA38680.1; -.								
DR	HSSP; P01679; 2FBJ.								
DR	InterPro; IPR003006; Ig_MHC.								
DR	InterPro; IPR003596; Ig_v.								
DR	Pfam; PF00047; ig; 1.								
DR	SMART; SM00406; IGV; 1.								
KW	Immunoglobulin V region; Hybridoma.								
FT	DOMAIN 1 23								
FT	DOMAIN 24 33								
FT	DOMAIN 34 48								
FT	DOMAIN 49 55								
FT	DOMAIN 56 87								
FT	DOMAIN 88 96								
FT	DOMAIN 97 106								
FT	DISULFID 23 87								
FT	NON_TER 107 107								
SQ	SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68E6 CRC64;								
Query Match 82.8%; Score 462; DB 1; Length 107;									
Best Local Similarity 84.0%; Pred. No. 1.7e-39;									
Matches 89; Conservative 7; Mismatches 10; Indels 0; Gaps 0;									
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Db	2	IVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQKSGTSPKRWIYDTSKLASGVPA	61						
Oy	62	SGSGSGTYSYLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEIKR	107						


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FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match
Best Local Similarity 76.9%; Score 429; DB 1; Length 107;
Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSAPGKVKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNSLASGVPAR 60
:| ||||| :|| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPIWYEISKLASGVPAR 60

QY 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYP-FTFGSGTKLEIKR 107
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 FSGSGGTSYSLTISRMEAEADAATYYCQQ-WNYPLITFGGGTKLEIKR 107

RESULT 10
KV6C_MOUSE
ID KV6C_MOUSE STANDARD; PRT; 107 AA.
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 601).
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).
RN [2]
RP SEQUENCE (TEPC 191).
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -!- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
THAT BIND GALACTAN.
DR PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match
Best Local Similarity 76.7%; Score 428; DB 1; Length 107;
Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSAPGKVKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNSLASGVPAR 60
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Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPIWYEISKLASGVPAR 60
:| ||||| :|| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYP-FTFGSGTKLEIKR 107
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 FSGSGGTSYSLTISRMEAEADAATYYCQQ-WNYPLITFGAGTKLEIKR 107

RESULT 11
KV6E_MOUSE
ID KV6E_MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; PubMed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR PIR; A01942; KVM5J5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87
FT STRAND 4 7
FT STRAND 10 14
FT TURN 15 16
FT STRAND 19 25
FT STRAND 31 37
FT TURN 39 40
FT STRAND 44 48
FT TURN 49 51
FT STRAND 52 53
FT TURN 55 56
FT TURN 59 60
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 74
FT HELIX 79 81
FT STRAND 83 91
FT TURN 92 93
FT STRAND 94 97
FT STRAND 101 106
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;
```


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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 44.7907 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIELTQSPAIMSASPGKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	502	90.0	134	11	Q8VDD0	Q8vdd0 mus musculu
2	470	84.2	106	5	Q9U410	Q9u410 schistosoma
3	442	79.2	235	11	Q91W12	Q91w12 mus musculu
4	434.5	77.9	97	11	Q9JL76	Q9jl76 mus musculu
5	403.5	72.3	101	11	Q9JL78	Q9jl78 mus musculu
6	380.5	68.2	234	11	Q8R062	Q8r062 mus musculu
7	371.5	66.6	214	11	Q9R1A5	Q9rla5 mus musculu
8	365.5	65.5	108	4	Q9UL77	Q9ul77 homo sapien
9	365.5	65.5	111	11	Q920E9	Q920e9 mus musculu
10	361	64.7	107	4	Q96SA9	Q96sa9 homo sapien
11	361	64.7	109	4	Q9UL78	Q9ul78 homo sapien
12	359.5	64.4	108	4	Q9UL70	Q9ul70 homo sapien
13	357.5	64.1	108	4	Q9UL79	Q9ul79 homo sapien
14	356.5	63.9	234	11	Q91WF8	Q91wf8 mus musculu
15	356.5	63.9	234	11	Q8VCP0	Q8vcp0 mus musculu
16	354.5	63.5	233	11	Q91WS9	Q91ws9 mus musculu

17	353	63.3	107	4	Q9UL81	Q9ul81 homo sapien
18	351.5	63.0	298	11	Q9QYF0	Q9qyf0 mus musculu
19	347.5	62.3	109	11	Q920E6	Q920e6 mus musculu
20	346.5	62.1	108	4	Q9UL83	Q9ul83 homo sapien
21	342.5	61.4	107	11	Q9JL84	Q9jl84 mus musculu
22	342	61.3	109	4	Q9UL86	Q9ul86 homo sapien
23	337.5	60.5	108	11	Q8VIJ0	Q8vij0 mus musculu
24	337	60.4	109	4	Q9UL85	Q9ul85 homo sapien
25	331	59.3	238	11	Q99M37	Q99m37 mus musculu
26	323	57.9	238	11	Q8VCI6	Q8vci6 mus musculu
27	321.5	57.6	127	11	Q925S9	Q925s9 mus musculu
28	320.5	57.4	116	4	Q96PF6	Q96pf6 homo sapien
29	313	56.1	239	11	Q8VC55	Q8vc55 mus musculu
30	308.5	55.3	103	11	Q9JL80	Q9jl80 mus musculu
31	307	55.0	239	4	Q8TCD0	Q8tcd0 homo sapien
32	300.5	53.9	107	11	Q9ERZ9	Q9erz9 mus musculu
33	297	53.2	104	11	Q9JL82	Q9jl82 mus musculu
34	295.5	53.0	114	4	Q9UL80	Q9ul80 homo sapien
35	295	52.9	241	11	Q921A6	Q921a6 mus musculu
36	292.5	52.4	99	11	Q9JL74	Q9jl74 mus musculu
37	286.5	51.3	234	11	Q8R028	Q8r028 mus musculu
38	281	50.4	237	4	Q8WTU6	Q8wtu6 homo sapien
39	276	49.5	237	4	Q8WUK4	Q8wuk4 homo sapien
40	260.5	46.7	109	6	Q9NOW5	Q9n0w5 oryctolagus
41	259	46.4	233	4	Q8TBC9	Q8tbc9 homo sapien
42	247.5	44.4	236	4	Q96E61	Q96e61 homo sapien
43	244	43.7	107	4	Q9NSD6	Q9nsd6 homo sapien
44	244	43.7	110	4	Q8TE63	Q8te63 homo sapien
45	243	43.5	108	4	Q96SB0	Q96sb0 homo sapien

ALIGNMENTS

RESULT 1

Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.

AC Q8VDD0;

DT 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Anti-MOG Z12 variable light chain (Fragment).

GN ANTI-MOG KAPPA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RA Chernajovsky Y.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RA Sembi P.;

RT "Targeting T cells to the CNS."

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ416331; CAC94866.1; -

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IGv; 1.

FT NON_TER 134

SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 90.0%; Score 502; DB 11; Length 134;
Best Local Similarity 89.7%; Pred. No. 3.8e-45;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVPARF 61

Db 24 IVLTQSPAIMASPGKVTMTCSASSISYMHWFQKPGTSPKRWIYDTSKLASGVPARF 83
QY 62 SGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
Db 84 SGSGGTSYSLTISRMEAEADAATYYCHQRSSYPWTFGGGTKLEIKRA 130

RESULT 2
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 84.2%; Score 470; DB 5; Length 106;
Best Local Similarity 87.4%; Pred. No. 6.5e-42;
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVPAFSG 63
Db 4 LTQSPAIMASPGKVTMTCSASSSVSYVYWLQKPGSPRLLIYDTNLSAGVPAFSG 63

QY 64 SGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 64 SGSGTSYSLTISRMEAEADAATYYCQQTSTYPTFGSGTKLEIK 106

RESULT 3
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 79.2%; Score 442; DB 11; Length 235;
Best Local Similarity 81.3%; Pred. No. 1.5e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVPAF 61
Db 24 IVLTQSPAIMASPGKVTMTCSASSSVSHHWYQKSGTSPKRWIYDTFKLTSGVPDRF 83

QY 62 SGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
Db 84 SGSGGTSYSLTISRMEAEADVATYYCQQWSRNPPTFGVGTKLEIKRA 130

RESULT 4
Q9JL76
ID Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;

Query Match 77.9%; Score 434.5; DB 11; Length 97;
Best Local Similarity 86.6%; Pred. No. 3.1e-38;
Matches 84; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 11 MSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVPAFSGSGGTSY 70
Db 1 LSASPGKVTMTCRASSSVSYMHWFQKPGSSPKWIYATNLSAGVPAFSGSGGTSY 60

QY 71 SLTISRMEAEADAATYYCQQRSS-YPTFGSGTKLEIK 106
Db 61 SLTISRVEAEADAATYYCQWSSSKYMYTFGGGTKLEIK 97

RESULT 5
Q9JL78
ID Q9JL78 PRELIMINARY; PRT; 101 AA.
AC Q9JL78;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

[illegible]

RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 64.4%; Score 359.5; DB 4; Length 108;
Best Local Similarity 63.9%; Pred. No. 2.7e-30;
Matches 69; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

QY 1 DIELTQSPAIMASAPGEKVTITCSASSVS-YMHWFQOKPGTSPKLIYSTNLASGVPA 59
||:||||: :||| |:||||| || :| |:|:||||| || ||: | | ||||:
Db 1 DIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQKPKGKPKSLIYAASTLQSGVPS 60

QY 60 RFGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEIKR 107
||||||||| :||||| :| ||||||| :| | ||| |||||||
Db 61 RFGSGSGTDFTLTISSLPEDVATYYCQKYNAPRTFGPGTKLEIKR 108

RESULT 13
Q9UL79
ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 64.1%; Score 357.5; DB 4; Length 108;
Best Local Similarity 62.0%; Pred. No. 4.4e-30;
Matches 67; Conservative 21; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIELTQSPAIMASAPGEKVTITCSASSV-SYMHWFQOKPGTSPKLIYSTNLASGVPA 59
||:||||: :||| |:||||| || :| |:|:||||| || ||: | | ||||:
Db 1 DIVMTQSPSSLSASTGDRVTISCRMSQGISSYLAWYQKPKGKAPPELLIYAASTLQSGVPS 60

QY 60 RFGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEIKR 107
||||||||| :||||| :||| ||||||| | :| ||| |||||||
Db 61 RFGSGSGTDFTLTISCIQSEDEATYYCQYYSFPTFGQGTKVEIKR 108

RESULT 14
Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAHL5292.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 63.9%; Score 356.5; DB 11; Length 234;
Best Local Similarity 63.3%; Pred. No. 1.4e-29;
Matches 69; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 DIELTQSPAIMASAPGEKVTITCSASSVS-YMHWFQOKPGTSPKLIYSTNLASGVPA 59
||:||||: :||| |:||||| || :| |:|:||||| :| | ||| | |||:
Db 21 DIQMTQTSSLSASGLGDRVTISCRASQDISNYLNWYQKPDGTVKLLIYTSRLYLGVPS 80

QY 60 RFGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEIKRA 108
||||||||| ||||||| :| | |||: ||| :| ||||||| |||: |||
Db 81 RFGSGSGTDYSLTISNLEQEDIATYFCQOGNTPPFTFGSGTKLEVKRA 129

RESULT 15
Q8VCP0
ID Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAHL9474.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 63.9%; Score 356.5; DB 11; Length 234;
Best Local Similarity 63.3%; Pred. No. 1.4e-29;
Matches 69; Conservative 15; Mismatches 24; Indels 1; Gaps 1;

Qy 1 DIELTQSPAIMSAPGEKVTITCSASSV-SYMHWFQOKPGTSPKLWIYSTSNLASGVA 59
Db 21 DIQLTQSPASLSASVGETVTITCRASENIYSYLAWYQOKGKSPQLLVYNKTLADGVPS 80
Qy 60 RFGSGSGTYSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
Db 81 RFGSGRSGTQFSLKINSLOPEDFGSYCQHHSGIPFTFGSGTKLEIKRA 129

Search completed: December 23, 2002, 07:29:56
Job time : 45.7907 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 9.12597 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	17	AAE13138	Humanised antibody
2	101	100.0	17	AAB82704	VEGF antagonist an
3	101	100.0	17	AAU74416	Heavy chain comple
4	101	100.0	117	AAE13143	Humanised antibody
5	101	100.0	117	AAB82709	VEGF antagonist an
6	101	100.0	117	AAU74417	Antigen-binding pr
7	101	100.0	136	AAE13145	Chimeric p1C11 hea
8	101	100.0	136	AAB82701	VEGF antagonist an
9	101	100.0	238	AAU74420	Antigen-binding pr
10	94	93.1	17	AAW89162	Anti-p53 monoclonal

11	94	93.1	17	21	AAV97230	Complementary dete
12	94	93.1	17	23	AAU74407	Heavy chain comple
13	94	93.1	20	21	AAV70794	Murine anti-p53 PA
14	94	93.1	112	20	AAW89173	Murine anti-p53 monoclonal
15	94	93.1	116	21	AAV70787	Murine anti-p53 mo
16	94	93.1	117	21	AAV97235	Variable heavy cha
17	94	93.1	117	23	AAU74412	Antigen-binding pr
18	94	93.1	122	20	AAV39531	Humanised Murine C
19	94	93.1	124	15	AAV60565	Anti-carcinobry
20	94	93.1	124	15	AAV60566	Anti-carcinobry
21	94	93.1	124	20	AAV39528	Murine COL1 VH cha
22	94	93.1	124	20	AAV39530	Humanised Murine C
23	94	93.1	124	20	AAV39536	Humanised Murine C
24	94	93.1	124	20	AAV39537	Humanised Murine C
25	94	93.1	124	20	AAV39538	Humanised Murine C
26	94	93.1	124	20	AAV39539	Humanised Murine C
27	94	93.1	124	20	AAV39540	Humanised Murine C
28	94	93.1	124	20	AAV39541	Humanised Murine C
29	94	93.1	124	20	AAV39542	Humanised Murine C
30	94	93.1	124	20	AAV39543	Humanised Murine C
31	94	93.1	124	23	AAU76632	Murine Col-1(CDA a
32	94	93.1	124	23	AAU76634	Humanised COL-1(CE
33	94	93.1	124	23	AAU76635	Humanised COL-1(CE
34	94	93.1	124	23	AAU76636	Humanised COL-1(CE
35	94	93.1	124	23	AAU76637	Humanised COL-1(CE
36	94	93.1	124	23	AAU76638	Humanised COL-1(CE
37	94	93.1	124	23	AAU76639	Humanised COL-1(CE
38	94	93.1	124	23	AAU76640	Humanised COL-1(CE
39	94	93.1	124	23	AAU76641	Humanised COL-1(CE
40	94	93.1	124	23	AAU76642	Humanised COL-1(CE
41	94	93.1	124	23	AAU76643	Humanised COL-1(CE
42	94	93.1	124	23	AAU76650	Protein template u
43	94	93.1	240	23	AAU74419	Antigen-binding pr
44	94	93.1	243	19	AAW60769	Single chain antib
45	94	93.1	270	16	AAV75719	MFE-23 antibody.

ALIGNMENTS

RESULT 1
AAE13138

ID AAE13138 standard; peptide; 17 AA.

XX AAE13138;

XX 28-JAN-2002 (first entry)

XX Humanised antibody murine heavy chain hypervariable region (VH) CDR2.

DE Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytotstatic; heavy chain hypervariable region; VH; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.

OS Mus sp.

XX WO200174296-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.

XX N-PSDB; AAD21664.

XX

PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 14; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumor cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody murine heavy chain hypervariable region (VH) CDR-2 used in the
CC exemplification of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 101; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFGQ 17
| | | | | | | | | | | | | | | | | |
Db 1 WIDPENGSDYAPKFGQ 17

RESULT 2
AAB82704
ID AAB82704; standard; Peptide; 17 AA.

XX
AC AAB82704;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 VH CDR-2.

XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumor; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumor; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
KW complementarity determining region.

XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.

XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -

XX
PS Disclosure; Page 37; 42pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 2 of the heavy chain variable region (see also AAB82701) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 101; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFGQ 17
| | | | | | | | | | | | | | | | | |
Db 1 WIDPENGSDYAPKFGQ 17

RESULT 3
AAU74416
ID AAU74416 standard; peptide; 17 AA.

XX
AC AAU74416;
XX
DT 26-MAR-2002 (first entry)

XX Heavy chain complementarity determining region H2 (CDRH2) version #2.
DE
XX Complementarity determining region; CDR; CDRH2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody heavy chain variable domain.

XX
OS SMus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20287.

XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 59; Page 60; 64pp; English.

CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; blocking VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the heavy chain variable domain
CC complementarity determining region H2 (CDRH2) version #2 incorporated
CC into an antigen-binding protein described in the method of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 101; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | |
Db 1 WIDPENGSDYAPKFG 17

RESULT 4
AAE13143
ID AAE13143 standard; Protein; 117 AA.

XX AAE13143;
AC AAE13143;
XX 28-JAN-2002 (first entry)
XX Humanised antibody heavy chain fragment.
DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.

XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.

XX WO200174296-A2.
PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.
DR N-PSDB; AAD21669.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -

XX Claim 8; Page 15; 68pp; English.

XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain fragment used in the exemplification of the
CC invention.

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | |
Db 50 WIDPENGSDYAPKFG 66

RESULT 5
AAB82709
ID AAB82709 standard; Protein; 117 AA.

XX AAB82709;

XX 15-OCT-2001 (first entry)

XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.

XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.

XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers
FT Region 26..35
FT /label= CDR-H1

FT /note= "complementarity determining region 1"

FT Region 50..66
FT /label= CDR-H2

FT /note= "complementarity determining region 2"

FT Region 99..106
FT /label= CDR-H3

FT /note= "complementarity determining region 3"

XX WO200154723-A1.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US02839.

XX 28-JAN-2000; 2000US-0178791.

XX 31-MAR-2000; 2000US-0539692.

XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Kerbel R;

XX WPI; 2001-514531/56.

DR N-PSDB; ANH26405.

XX Treating or controlling an angiogenic dependent condition (e.g. a

PT neoplasm; collagen-vascular or autoimmune disease) in mammal by

PT administering a combination of an antiangiogenic molecule and a

PT chemotherapeutic agent

XX

PS Disclosure; Page 38; 42pp; English.

XX

CC The present sequence is that of the heavy chain variable region of

CC IMC-1C11, a mouse-human chimeric antibody that has vascular

CC endothelial growth factor (VEGF) antagonist activity. The antibody,

CC or a fragment of it, can be used as an anti-angiogenic molecule,

CC together with a chemotherapeutic acid, for the treatment of an

CC angiogenic dependent condition in a mammal, especially a human.

CC The invention relates generally to a method of treating or

CC controlling an angiogenic dependent condition by administering an

CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a

CC regression or arrest of the condition while minimising or

CC preventing significant toxicity of the chemotherapeutic agent.

CC The anti-angiogenic molecule inhibits or blocks the action of a

CC vascular endothelium survival factor such as VEGF or its receptor,

CC and is especially IMC-1C11. Conditions that can be treated include

CC a neoplasm, a collagen-vascular disease or an autoimmune disease,

CC especially a solid tumour, including breast carcinoma, lung

CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,

CC ovarian carcinoma, neuroblastoma, central nervous system tumour,

CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 22; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17

Db 50 WIDPENGSDYAPKFG 66

RESULT 6

AAU74417

ID AAU74417 standard; peptide; 117 AA.

XX

AC AAU74417;

XX

DT 26-MAR-2002 (first entry)

XX

DE Antigen-binding protein heavy chain variable domain (VH) #2.

XX

KW Antigen-binding protein; antibody heavy chain variable domain;

KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.

XX

OS Mus sp.

XX

PN WO200190192-A2.

XX

PD 29-NOV-2001.

XX

PF 24-MAY-2001; 2001WO-US16924.

XX

PR 24-MAY-2000; 2000US-206749P.

XX

PA (IMCL) IMCLONE SYSTEMS INC.

XX

PI Zhu Z;

XX

WPI; 2002-106189/14.

DR N-PSDB; AAS20288.

XX

PT New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX Claim 61; Page 60; 64pp; English.

XX

CC The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

CC light chain constant domain (CL domain), and P2 has an antigen-binding

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC neutralising the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This sequence represents a heavy chain variable domain (VH) incorporated

CC into Fv, an engineered protein containing a heavy chain variable domain

CC and a light chain variable domain in one polypeptide chain, described in

CC the method of the invention.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17

Db 50 WIDPENGSDYAPKFG 66

RESULT 7

AAE13145

ID AAE13145 standard; Protein; 136 AA.

XX

AC AAE13145;

XX

DT 28-JAN-2002 (first entry)

XX

DE Chimeric p1C11 heavy chain fragment.

XX

KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;

KW cytosstatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;

KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;

KW human; p1C11 vector.

XX

OS Chimeric - Homo sapiens.

OS Chimeric - Unidentified.

XX

FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Leader_peptide

FT /note= "Mature chimeric p1C11 heavy chain fragment"

FT Region 20..136

FT /label= CDR_H1

FT Region 45..54

FT /label= CDR_H2

FT Misc-difference 84

FT /note= "Residue 'O' is present at this location in the

FT sequence shown in fig-11 of the specification"

FT Misc-difference 101

FT /note= "Residue 'O' is present at this location in the

FT sequence shown in fig-11 of the specification"


```
FT Region 119..125
FT /label= CDR_H3
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Witte L, Rafii S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21682.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC pIC11 heavy chain fragment which is used for the construction of chimeric
CC pIC11 IgG expression vector. Chimeric pIC11 heavy chain contains cloned
CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
CC domain (CH).
XX
SQ Sequence 136 AA;
Query Match 100.0%; Score 101; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDSYAPKFGQ 17
| | | | | | | | | | | | | | |
Db 69 WIDPENGSDSYAPKFGQ 85
RESULT 8
AAB82701
ID AAB82701 standard; Protein; 136 AA.
XX
AC AAB82701;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
```

```
PH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..136
FT /label= Mature_protein
FT Region 45..54
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 59..85
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 118..125
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
XX WO200154723-A1.
PN
XX 02-AUG-2001.
PD
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26413.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
PS Disclosure; Fig 1; 42pp; English.
XX
CC The present sequence is that of the heavy chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 136 AA;
Query Match 100.0%; Score 101; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDSYAPKFGQ 17
| | | | | | | | | | | | | | |
Db 69 WIDPENGSDSYAPKFGQ 85
RESULT 9
AAU74420
ID AAU74420 standard; Protein; 238 AA.
```


XX AC AAU74420;
XX DT 26-MAR-2002 (first entry)
XX DE Antigen-binding protein, single chain variable fragment version #2.
XX KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX OS Mus sp.
OS Synthetic
XX FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 61"
FT Region 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable fragment
FT protein. Encoded by AAS20285"
FT Region 133..238
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 61"
XX PN WO200190192-A2.
XX PD 29-NOV-2001.
XX PF 24-MAY-2001; 2001WO-US16924.
XX PR 24-MAY-2000; 2000US-206749P.
XX PA (IMCL-) EMCLONE SYSTEMS INC.
XX PI Zhu Z;
XX DR WPI; 2002-106189/14.
XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX PS Claim 63; Page 62-63; 64pp; English.
XX CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv); an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
CC invention.

XX SQ Sequence 238 AA;
XX Query Match 100.0%; Score 101; DB 23; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFOG 17
Db 50 WIDPENGSDYAPKFOG 66
RESULT 10
AAW89162
ID AAW89162 standard; peptide; 17 AA.
XX AC AAW89162;
XX DT 25-MAR-1999 (first entry)
XX DE Anti-p53 monoclonal antibody 421 CDR2 heavy chain based peptide.
XX KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.
XX OS Mus sp.
OS Synthetic.
XX PN WO9856416-A1.
XX PD 17-DEC-1998.
XX PF 09-JUN-1998; 98WO-IL00266.
XX PR 09-JUN-1997; 97IL-0121041.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
PI Wolkowicz R;
XX DR WPI; 1999-070296/06.
XX PT Use of a monoclonal antibody to a tumour-associated antigen - to
PT induce anti-tumour immunity or elicit an increased immune response
PT to the antigen
XX PS Claim 7; Page 29; 47pp; English.
XX CC The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarity determining region) on the heavy or light chain of Mab
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of Mab, in a gene delivery vehicle. The present
CC sequence represents a peptide based on CDR2 of the heavy chain of
CC anti-p53 Mab 421. Also described is a method for generating sequence-
CC specific, anti-DNA antibodies (Ab) by immunising a mammal with a Mab
CC directed to a domain containing a DNA-binding site of a DNA-binding
CC protein. (A) is used to treat a wide variety of primary and metastatic
CC cancers, particularly those where p53 is involved. Ab are used for
CC diagnosis (e.g to determine critical sequences in animal or plant
CC breeding); to identify bacteria and other parasites; to determine
CC parentage; in forensic science; to isolate specific genes for DNA
CC vaccination; in gene sequencing and cloning; also possibly for activation
CC of selected therapeutic genes in plants, animals and humans. (A) induce
CC an effective anti-tumour response without causing harm to the patient.
CC The method uses (A) to generate anti-TAA by exploiting the anti-idiotypic
CC network.
XX SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 20; Length 17;
Best Local Similarity 88.2%; Pred. No. 5.6e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 WIDPENGDEYAPKFQ 17
| | | | | | | | | | | | | | | | | | | | | |

RESULT 11
AA97230
ID AA97230 standard; Protein; 17 AA.
XX
AC AA97230;
XX
DT 19-DEC-2000 (first entry)
XX
DE Complementary determining region (CDRH2) of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;
XX
DR WPI; 2000-505966/45.
DR N-PSDB; AAA53762.

Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth

Claim 3; Page 50; 55pp; English.

New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Kaposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the immunoglobulins of the invention.

Sequence 17 AA;

Query Match 93.1%; Score 94; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-08;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFQ 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 WIDPENGSDYAPKFQ 17
| | | | | | | | | | | | | | | | | | | | | |

RESULT 12
AAU74407
ID AAU74407 standard; peptide; 17 AA.
XX
AC AAU74407;
XX
DT 26-MAR-2002 (first entry)
XX
DE Heavy chain complementarity determining region H2 (CDRH2) version #1.
XX
KW Complementarity determining region; CDR; CDRH2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody heavy chain variable domain.
XX
OS Mus sp.

XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.

XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.

XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;

XX
DR WPI; 2002-106189/14.

DR N-PSDB; AAS20278.

XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides

PS Claim 55; Page 56; 64pp; English.

XX
CC The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This peptide sequence represents the heavy chain variable domain complementarity determining region H2 (CDRH2) version #1 incorporated into an antigen-binding protein described in the method of the invention.

XX
SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 23; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WIDPENGDSYAPKFG 17
|||||
Db 1 WIDPENGDSGYAPKFG 17

RESULT 13
AAY70794
ID AAY70794 standard; peptide; 20 AA.
XX
AC AAY70794;
XX

DT 31-JUL-2000 (first entry)
XX

DE Murine anti-p53 PAb-421 mAb heavy chain CDR based peptide PAb-421 H2.
XX
KW Murine; p53 protein; monoclonal antibody; mAb; PAb-421; PAb-421 H2;
KW heavy chain variable region; VH; complementarity determining region; CDR;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW DNA-binding domain.

OS Mus sp.

XX WO200023082-A1.

PN 27-APR-2000.

PD 19-OCT-1999; 99WO-US24443.

XX 19-OCT-1998; 98US-0104816.

PA (YEDA) YEDA RES & DEV CO LTD.

XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;

XX WPI; 2000-339512/29.

DR Treatment of systemic lupus erythematosus by down-regulating the
XX autoimmune response to the C-terminal DNA-binding domain of the p53
PT protein by an active compound comprising of antibodies to p53 or
PT fragments of p53 -

XX Claim 78; Fig 10; 87pp; English.

XX The patent discloses a method for the treatment of systemic lupus
CC erythematosus (SLE) by down-regulating the autoimmune response to the
CC C-terminal DNA-binding domain of p53 protein by an active compound.
CC The present sequence is a PAb-421 H2 peptide which comprises the
CC complementarity determining region (CDR) of the heavy chain of a
CC monoclonal antibody PAb-421 which is specific to the C-terminal
CC DNA-binding domain of murine p53 protein. The peptide corresponds to
CC residues 48-67 of PAb-421 heavy chain variable region. It is an
CC example of the active compound useful in the diagnosis, prevention
CC and treatment of SLE in humans.

XX Sequence 20 AA;

Query Match 93.1%; Score 94; DB 21; Length 20;
Best Local Similarity 88.2%; Pred. NO. 6.6e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WIDPENGDSYAPKFG 17
|||||
Db 3 WIDPENGDTYAPKFG 19

RESULT 14
AAW89173
ID AAW89173 standard; peptide; 112 AA.
XX
AC AAW89173;

XX

DT 25-MAR-1999 (first entry)
XX
DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
XX
KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.

XX Mus sp.

OS Synthetic.

XX WO9856416-A1.

PN 17-DEC-1998.

XX 09-JUN-1998; 98WO-IL00266.

XX 09-JUN-1997; 97IL-0121041.

PA (YEDA) YEDA RES & DEV CO LTD.

XX Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;

PI Wolkowicz R;

XX WPI; 1999-070296/06.

DR Use of a monoclonal antibody to a tumour-associated antigen - to

XX induce anti-tumour immunity or elicit an increased immune response

XX to the antigen

PS Example 3; Fig 3; 47pp; English.

XX The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (mAb) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarity determining region) on the heavy or light chain of mAb
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of mAb, in a gene delivery vehicle. The present
CC sequence represents the variable heavy chain sequence from anti-p53 mAb
CC 421. Also described is a method for generating sequence-specific,
CC anti-DNA antibodies (Ab) by immunising a mammal with a mAb directed to a
CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
CC used to treat a wide variety of primary and metastatic cancers,
CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
CC to determine critical sequences in animal or plant breeding); to
CC identify bacteria and other parasites; to determine parentage; in
CC forensic science; to isolate specific genes for DNA vaccination; in gene
CC sequencing and cloning; also possibly for activation of selected
CC therapeutic genes in plants, animals and humans. (A) induce an effective
CC anti-tumour response without causing harm to the patient. The method
CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.

XX Sequence 112 AA;

Query Match 93.1%; Score 94; DB 20; Length 112;
Best Local Similarity 88.2%; Pred. NO. 4.2e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WIDPENGDSYAPKFG 17
|||||
Db 47 WIDPENGDTYAPKFG 63

RESULT 15
AAY70787
ID AAY70787 standard; Protein; 116 AA.

XX AAY70787;

AC 31-JUL-2000 (first entry)

XX Murine anti-p53 monoclonal antibody PAb-421 heavy chain variable region.

XX Murine; p53 protein; monoclonal antibody; PAb-421; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW heavy chain variable region; VH; complementarity determining region; CDR.
XX

OS Mus sp.

XX
FH Key Location/Qualifiers
FT Region 26..35
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region 50..56
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region 99..105
FT /label= CDR
FT /note= "Complementarity determining region"
XX

PN WO200023082-A1.

XX 27-APR-2000.

PF 19-OCT-1999; 99WO-US24443.

PR 19-OCT-1998; 98US-0104816.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;

PI WPI; 2000-339512/29.

XX
PT Treatment of systemic lupus erythematosus by down-regulating the
PT autoimmune response to the C-terminal DNA-binding domain of the p53
PT protein by an active compound comprising of antibodies to p53 or
PT fragments of p53 -
XX

PS Claim 78; Fig 9; 87pp; English.

XX
CC The patent discloses a method for the treatment of systemic lupus
CC erythematosus (SLE) by down-regulating the autoimmune response to the
CC C-terminal DNA-binding domain of p53 protein by an active compound.
CC The present sequence is a heavy chain variable region of monoclonal
CC antibody PAb-421 which is specific to the C-terminal DNA-binding domain
CC of murine p53 protein. PAb-421 antibody and peptides based on
CC complementarity determining regions of light and heavy chain variable
CC regions of the antibody, are examples of active compounds useful in the
CC diagnosis, prevention and treatment of SLE in humans.
XX

SQ Sequence 116 AA;

Query Match 93.1%; Score 94; DB 21; Length 116;
Best Local Similarity 88.2%; Pred. No. 4.4e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17

Db |||||:|||||

50 WIDPENGTEYAPKFOG 66

Search completed: December 23, 2002, 07:25:09
Job time : 9.12597 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 3.06395 Seconds
(without alignments)
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Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDSYAPKFGQ 17

Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	93.1	124	1	US-08-017-570-4
2	94	93.1	124	1	US-08-017-570-6
3	94	93.1	124	1	US-08-471-426-4
4	94	93.1	124	1	US-08-471-426-6
5	94	93.1	124	4	US-09-672-609-1
6	94	93.1	124	4	US-09-672-609-3
7	94	93.1	124	4	US-09-672-609-4
8	94	93.1	124	4	US-09-672-609-5
9	94	93.1	124	4	US-09-672-609-6
10	94	93.1	124	4	US-09-672-609-7
11	94	93.1	124	4	US-09-672-609-9
12	94	93.1	124	4	US-09-672-609-10
13	94	93.1	124	4	US-09-672-609-11
14	94	93.1	124	4	US-09-672-609-12
15	94	93.1	124	4	US-09-672-609-12
16	94	93.1	124	4	US-09-025-403A-1
17	94	93.1	124	4	US-09-025-403A-3
18	94	93.1	124	4	US-09-025-403A-4
19	94	93.1	124	4	US-09-025-403A-5
20	94	93.1	124	4	US-09-025-403A-6
21	94	93.1	124	4	US-09-025-403A-7
22	94	93.1	124	4	US-09-025-403A-8
23	94	93.1	124	4	US-09-025-403A-9
24	94	93.1	124	4	US-09-025-403A-10
25	94	93.1	124	4	US-09-025-403A-11
26	94	93.1	124	4	US-09-025-403A-12
27	94	93.1	124	5	PCT-US94-01709-4

28	94	93.1	124	5	PCT-US94-01709-6	Sequence 6, Appli
29	94	93.1	270	2	US-08-652-507-2	Sequence 2, Appli
30	94	93.1	535	4	US-08-983-035A-38	Sequence 38, Appl
31	94	93.1	553	2	US-08-661-052-16	Sequence 16, Appl
32	94	93.1	553	4	US-09-188-082-16	Sequence 16, Appl
33	94	93.1	553	4	US-09-364-088-16	Sequence 16, Appl
34	94	93.1	553	4	US-09-102-716-16	Sequence 16, Appl
35	90	89.1	17	4	US-09-171-945-31	Sequence 31, Appl
36	90	89.1	120	4	US-09-171-945-11	Sequence 11, Appl
37	90	89.1	120	4	US-09-171-945-55	Sequence 55, Appl
38	90	89.1	120	4	US-09-171-945-75	Sequence 75, Appl
39	90	89.1	120	4	US-09-171-945-79	Sequence 79, Appl
40	90	89.1	120	4	US-09-171-945-81	Sequence 81, Appl
41	90	89.1	120	4	US-09-171-945-85	Sequence 85, Appl
42	90	89.1	120	4	US-09-171-945-89	Sequence 89, Appl
43	90	89.1	120	4	US-09-171-945-91	Sequence 91, Appl
44	90	89.1	255	4	US-09-171-945-19	Sequence 19, Appl
45	90	89.1	255	4	US-09-171-945-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-4

Query Match 93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDSYAPKFGQ 17
|||||:|||||
Db 50 WIDPENGDTYAPKFGQ 66

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RESULT 2
US-08-017-570-6
; Sequence 6, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-6

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66

RESULT 3
US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66

RESULT 4
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66
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ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66

RESULT 4
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66
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; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match 93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 5

US-09-672-609-1
; Sequence 1, Application US/09672609
; Patent No. 6333405

GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn

; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/672,609

; CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/025,403

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 1

; LENGTH: 124

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: Murine Col-1 VH

; LOCATION: 1..124

US-09-672-609-1

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 6

US-09-672-609-3
; Sequence 3, Application US/09672609
; Patent No. 6333405

GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn

; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/672,609

; CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/025,403

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 3

; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124

; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-3

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 7

US-09-672-609-4
; Sequence 4, Application US/09672609
; Patent No. 6333405

GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn

; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/672,609

; CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/025,403

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 4

; LENGTH: 124

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: Humanized COL-1 VH, HuVHA

; LOCATION: 1..124

; OTHER INFORMATION: Humanized heavy chain variable region containing human

; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-4

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | |
Db 50 WIDPENGDTYAPKFG 66

RESULT 8

US-09-672-609-5
; Sequence 5, Application US/09672609
; Patent No. 6333405

GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn

; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/672,609

; CURRENT FILING DATE: 2000-09-28

;
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-672-609-5

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 9
US-09-672-609-6
; Sequence 6, Application US/09672609
; Patent No. 633405

;
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 6
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
US-09-672-609-6

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 10
US-09-672-609-7
; Sequence 7, Application US/09672609
; Patent No. 633405

;
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.

;
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
US-09-672-609-7

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 11
US-09-672-609-8
; Sequence 8, Application US/09672609
; Patent No. 633405

;
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 8
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHATAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGDTYAPKFG 66

RESULT 12
US-09-672-609-9
; Sequence 9, Application US/09672609
; Patent No. 633405

```

: GENERAL INFORMATION:
: APPLICANT: Anderson, W.H. Kerr
: APPLICANT: Tempest, Philip R.
: APPLICANT: Carr, Frank J.
: APPLICANT: Harris, William J.
: APPLICANT: Armour, Kathryn
: TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/672,609
: CURRENT FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 09/025,403
: PRIOR FILING DATE: 1998-02-18
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Microsoft Word 97 SR-2
: SEQ ID NO 9
: LENGTH: 124
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Humanized COL-1 VH, HuvHASTAY
: LOCATION: 1..124
: OTHER INFORMATION: Humanized heavy chain variable region containing human
: OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
: OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
: OTHER INFORMATION: Thr-98
: US-09-672-609-9

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Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. NO. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WIDPENGSDYAPKFQG 17
        | | | | | | | : | | | | |
Db     50 WIDPENGDEYAPKFQG 66
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RESULT 13
 US-09-672-609-10
 ; Sequence 10, Application US/09672609
 ; Patent No. 6333405
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, W.H. Kerr
 ; APPLICANT: Tempest, Philip R.
 ; APPLICANT: Carr, Frank J.
 ; APPLICANT: Harris, William J.
 ; APPLICANT: Armour, Kathryn
 ; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/672,609
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/025,403
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Microsoft Word 97 SR-2
 ; SEQ ID NO 10
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Humanized COL-1 VH, HuVHT
 ; LOCATION: 1..124
 ; * OTHER INFORMATION: Humanized heavy chain variable region containing human
 ; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
 ; OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
 US-09-672-609-10

```
QY      1 WIDPENGSDYAPKEFG 17
        ↑↑↑↑↑↑↑↑:↑↑↑↑↑↑
Db      50 WIDPENGDTYAPKEFG 66
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RESULT 14
 US-09-672-609-11
 ; Sequence 11, Application US/09672609
 ; Patent No. 6333405
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, W.H. Kerr
 ; APPLICANT: Tempest, Philip R.
 ; APPLICANT: Carr, Frank J.
 ; APPLICANT: Harris, William J.
 ; APPLICANT: Armour, Kathryn
 ; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/672,609
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/025,403
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Microsoft Word 97 SR-2
 ; SEQ ID NO 11
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Humanized COL-1 VH, HuVHS
 ; LOCATION: 1..124
 ; OTHER INFORMATION: Humanized heavy chain variable region containing human
 ; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
 ; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
 US-09-672-609-11

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQG 17
|||||:|||||
Db 50 WIDPENGDTYAPKFQG 66

RESULT 15
 US-09-609-12
 ; Sequence 12, Application US/09672609
 ; Patent No. 6333405
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, W.H. Kerr
 ; APPLICANT: Tempest, Philip R.
 ; APPLICANT: Carr, Frank J.
 ; APPLICANT: Harris, William J.
 ; APPLICANT: Armour, Kathryn
 ; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/672,609
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/025,403
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Microsoft Word 97 SR-2
 ; SEQ ID NO 12
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Humanized COL-1 VH, HuVHSTAY
 ; LOCATION: 1..124
 ; OTHER INFORMATION: Humanized heavy chain variable region expressed from AT
 ; OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL
 ; OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Thr-76, Thr-78, Ala
 ; OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
 US-09-672-609-12

Query Match 93.1%; Score 94; DB 4; Length 124;

Best Local Similarity 88.28; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFQG 17
|||||:|||||
Db 50 WIDPENGTEYAPKFQG 66

Search completed: December 23, 2002, 07:33:18
Job time : 3.06395 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 3.36047 seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDYAPKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	94	93.1	82	2	A36025	Ig heavy chain V r
2	86	85.1	118	2	S25174	Ig heavy chain V r
3	84	83.2	136	2	S04576	Ig heavy chain pre
4	82	81.2	116	2	S15672	Ig heavy chain V r
5	78	77.2	137	2	S52445	Ig heavy chain V r
6	68	67.3	143	1	ELHUND	Ig heavy chain pre
7	67	66.3	85	2	E37262	Ig heavy chain V r
8	64	63.4	86	2	S54912	Ig heavy chain V r
9	63	62.4	98	2	S26938	Ig heavy chain V r
10	63	62.4	98	2	S26912	Ig heavy chain V r
11	63	62.4	99	2	D37262	Ig heavy chain V r
12	63	62.4	107	2	PH1013	Ig heavy chain V r
13	63	62.4	108	2	PH1012	Ig heavy chain V r
14	63	62.4	117	2	S31680	Ig heavy chain V r
15	63	62.4	117	2	S18551	Ig heavy chain V r
16	63	62.4	118	2	S36265	Ig heavy chain V r
17	63	62.4	120	2	S03471	Ig heavy chain V-D
18	63	62.4	122	2	S06823	Ig heavy chain V r
19	63	62.4	123	2	D33548	Ig heavy chain V-1
20	63	62.4	123	2	PH1403	Ig heavy chain V r
21	63	62.4	129	2	S46393	Ig heavy chain V r
22	63	62.4	135	2	S49530	anti-Sm antibody V
23	62	61.4	178	2	S29594	Ig gamma chain (WM
24	61	60.4	120	2	S03484	Ig heavy chain V-D
25	61	60.4	221	2	S49220	Ig gamma-1 chain -
26	60	59.4	77	2	S46465	Ig heavy chain V r
27	60	59.4	98	2	S26918	Ig heavy chain V r
28	60	59.4	98	2	S26909	Ig heavy chain V r
29	60	59.4	132	2	S31596	Ig heavy chain V r

30	60	59.4	136	2	S31600	Ig heavy chain V r
31	59	58.4	86	2	S29544	Ig heavy chain V r
32	59	58.4	97	2	S16028	Ig heavy chain V r
33	59	58.4	98	2	S26921	Ig heavy chain V r
34	59	58.4	116	2	S24289	Ig gamma chain V r
35	58	57.4	114	2	PH1667	Ig heavy chain V r
36	58	57.4	118	2	PH1666	Ig heavy chain V r
37	57.5	56.9	98	2	S26911	Ig heavy chain V r
38	57	56.4	110	2	PH1670	Ig heavy chain V r
39	57	56.4	115	2	S03482	Ig heavy chain V-D
40	57	56.4	120	2	S31999	Ig heavy chain V r
41	57	56.4	171	2	S23623	Ig heavy chain V r
42	56	55.4	107	2	A27646	Ig heavy chain V r
43	56	55.4	126	2	I44151	Ig heavy chain V r
44	56	55.4	127	2	S34014	Ig heavy chain V r
45	55	54.5	99	2	C37262	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A36025

Ig heavy chain V region (PR8-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999

C:Accession: A36025; E36025

R:Caton, A.J.; Koprowski, H.

Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990

A:Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinator

A:Reference number: A36025; MUID:90349634; PMID:1696733

A:Accession: A36025

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-82 <CAT>

A:Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956

A>Note: PR8-1

A:Accession: E36025

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 19-82 <CA2>

A:Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964

A>Note: clone PR8-21

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 82;
Best Local Similarity 88.2%; Pred. No. 5.9e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17

|||||||:|||||

Db 12 WIDPENGDTYAPKFQ 28

RESULT 2

S25174

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S25174; S33133

R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.

Submitted to the EMBL Data Library, July 1992

A:Description: Structure and binding properties of monoclonal antibodies to core hist

A:Reference number: S25174

A:Accession: S25174

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MON>

A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259

A:Accession: S33133

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-118 <MO2>
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 86; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 1.7e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|:|:|
Db 50 WIDPENGDTYASKFG 66

RESULT 3

S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576

R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involveme
A;Reference number: S04573; MUID:87133856; PMID:3102255
A;Accession: S04576

A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 84; DB 2; Length 136;
Best Local Similarity 82.4%; Pred. No. 4.1e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|:|:|
Db 69 WIDPENGDTYASKFG 85

RESULT 4

S15672
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S15672

R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,
Bio/Technology 9, 266-271, 1991
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi
A;Reference number: S15672; MUID:91337412; PMID:1367535
A;Accession: S15672

A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-116 <TEM>

A;Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 7.2e-06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|:|:|
Db 50 WIDPENDDVQYAPKFG 66

RESULT 5

S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged
A;Reference number: S52445
A;Accession: S52445

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 78; DB 2; Length 137;
Best Local Similarity 76.5%; Pred. No. 3.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|:|:|
Db 69 WIDPENGTVYDPKFG 85

RESULT 6

E1HUND
Ig heavy chain precursor V-I region (Nd) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C;Accession: A93933; A02026

R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin
A;Reference number: A93933; MUID:83065234; PMID:6815656
A;Accession: A93933
A;Molecule type: mRNA
A;Residues: 1-143 <KEN>

R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A;Reference number: A94418
A;Contents: annotation; partial sequence
A;Note: this epsilon chain was isolated from a myeloma protein

C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>

F;30-113/Domain: immunoglobulin homology <IMM>
F;16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
F;37-111/Disulfide bonds: #status experimental

Query Match 67.3%; Score 68; DB 1; Length 143;
Best Local Similarity 58.8%; Pred. No. 0.0016;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
||||:|:|:|:|
Db 65 WINPNSGGTNYAPRFQ 81

RESULT 7

E37262
Ig heavy chain V region (6H2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-May-1997

C;Accession: E37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: E37262
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-85 <GOS>
A;Cross-references: GB:M57991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.3%; Score 67; DB 2; Length 85;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFQ 17
||| |||: | |||||
Db 29 IDPANGDTRYDPKFQ 44

RESULT 8
S54912
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S54912
R;Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G.
submitted to the EMBL Data Library, November 1992
A;Reference number: S54912
A;Accession: S54912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <TOM>
A;Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 86;
Best Local Similarity 64.7%; Pred. No. 0.0039;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFQ 17
||: | || | |||||
Db 38 WINPGNGSPSYAKKFQ 54

RESULT 9
S26938
Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0066;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFQ 17

Db 50 WINPNSGGTNYAQKFQ 66
||: | : | : | | |||||
RESULT 10
S26912
Ig heavy chain V region (DP-8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12310; NID:g32979; PIDN:CAA78180.1; PID:g32980
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0066;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFQ 17
||: | : | : | | |||||
Db 50 WINPNSGGTNYAQKFQ 66

RESULT 11
D37262
Ig heavy chain V region (2E5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: D37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D37262
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-99 <GOS>
A;Cross-references: GB:M57990; NID:g195046; PIDN:AAA63328.1; PID:g195047
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 99;
Best Local Similarity 68.8%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFQ 17
||| ||:: | |||||
Db 43 IDPANGNTRYDPKFQ 58

RESULT 12
PH1013
Ig heavy chain V region (clone 111.67) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1013
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1013
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA

A;Residues: 1-107 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 107;
Best Local Similarity 73.3%; Pred. No. 0.0073;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFQ 16
||| ||:: |||||
Db 51 IDPANGNTKYAPKFQ 65

RESULT 13
PH1012
Ig heavy chain V region (clone 17p.73) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1012
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 108;
Best Local Similarity 73.3%; Pred. No. 0.0073;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFQ 16
||| ||:: |||||
Db 51 IDPANGNTKYAPKFQ 65

RESULT 14
S31680
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31680
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CUI>
A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 117;
Best Local Similarity 58.8%; Pred. No. 0.008;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFQ 17
||:|:|:|:|
Db 69 WINPNSGGTNYAQKFQ 85

RESULT 15
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus:
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18551
A;Molecule type: DNA
A;Residues: 1-117 <SHI>
A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23625
A;Molecule type: DNA
A;Residues: 1-117 <OLE>
A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 117;
Best Local Similarity 58.8%; Pred. No. 0.008;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFQ 17
||:|:|:|:|
Db 69 WINPNSGGTNYAQKFQ 85

Search completed: December 23, 2002, 07:31:39
Job time : 4.36047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 1.68023 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	68	67.3	147	1 HV1C_HUMAN	P01744 homo sapien
2	52	51.5	117	1 HV1G_HUMAN	P23083 homo sapien
3	51	50.5	117	1 HV1B_HUMAN	P01743 homo sapien
4	51	50.5	350	1 NUD9_HUMAN	Q9bw91 homo sapien
5	47	46.5	1709	1 SN_HUMAN	Q9bzz2 homo sapien
6	46	45.5	117	1 HV12_MOUSE	P01756 mus musculu
7	46	45.5	117	1 HV13_MOUSE	P01757 mus musculu
8	46	45.5	117	1 HV52_MOUSE	P06327 mus musculu
9	46	45.5	118	1 HV51_MOUSE	P06330 mus musculu
10	45	44.6	1387	1 PUR4_ARATH	Q9m8d3 arabidopsis
11	44	43.6	402	1 MCE1_SCHPO	P40997 schizosacch
12	44	43.6	944	1 CHS2_NEUCR	P30589 neurospora
13	43	42.6	120	1 HV03_MOUSE	P01747 mus musculu
14	43	42.6	238	1 YIGB_ECOLI	P23306 escherichia
15	43	42.6	511	1 C772_SOLME	P37124 solanum mel
16	43	42.6	776	1 HYPF_AZOVI	P40596 azotobacter
17	43	42.6	977	1 DLP3_RAT	P97838 rattus norv
18	43	42.6	3329	1 BRC2_MOUSE	P97929 mus musculu
19	42	41.6	140	1 HV02_MOUSE	P01746 mus musculu
20	41.5	41.1	117	1 HV03_CAICR	P03982 caiman croc
21	41.5	41.1	551	1 YG1F_YEAST	P53214 saccharomyc
22	41.5	41.1	597	1 ETFD_CAEEL	Q11190 c probable
23	41	40.6	117	1 HV06_MOUSE	P01750 mus musculu
24	41	40.6	120	1 HV50_MOUSE	P06329 mus musculu
25	41	40.6	526	1 THRC_ARATH	Q9s7b5 arabidopsis
26	41	40.6	783	1 HELS_HALN1	Q9bmrv6 halobacteri
27	41	40.6	830	1 SREC_HUMAN	Q14162 homo sapien
28	41	40.6	977	1 DLP1_HUMAN	Q14490 homo sapien
29	41	40.6	992	1 DLP1_RAT	P97836 rattus norv
30	41	40.6	1005	1 EPA8_HUMAN	P29322 homo sapien
31	41	40.6	1338	1 PUR4_HUMAN	Q15067 homo sapien
32	41	40.6	1343	1 PUR4_CAEEL	Q19311 caenorhabdi
33	41	40.6	1354	1 PUR4_DROME	P35421 drosophila

34	41	40.6	1857	1 FAS2_PENPA	P15368 p fatty aci
35	40.5	40.1	205	1 DNBI_ADE12	P36704 human adeno
36	40	39.6	117	1 HV1A_HUMAN	P01742 homo sapien
37	40	39.6	156	1 RNP_HUMAN	P07998 homo sapien
38	40	39.6	227	1 YG24_HAEIN	P44276 haemophilus
39	40	39.6	254	1 MOXI_HUMAN	P50221 homo sapien
40	40	39.6	297	1 YMY9_YEAST	Q03161 saccharomyc
41	40	39.6	416	1 PAI2_RAT	P29524 rattus norv
42	40	39.6	496	1 PACR_MOUSE	P70205 mus musculu
43	40	39.6	523	1 PACR_RAT	P32215 rattus norv
44	40	39.6	712	1 GFAL_CANAL	P53704 candida alb
45	40	39.6	717	1 MTO1_HUMAN	Q9y2z2 homo sapien

ALIGNMENTS

RESULT 1					
HV1C_HUMAN					
ID	HV1C_HUMAN	STANDARD;	PRT;	147 AA.	
AC	P01744;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ig heavy chain V-I region ND precursor (Fragments).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83065234; PubMed=6815656;				
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,				
RA	Bell L.O., Gould H.J.;				
RT	"Cloning and sequence determination of the gene for the human				
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RN	[2]				
RP	SEQUENCE OF 20-147.				
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;				
RL	(In) Bach M.K. (eds.);				
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,				
RL	Marcel Dekker, New York (1978).				
CC	-I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA				
CC	PROTEIN.				
DR	PIR; A02026; ELHUND.				
DR	HSSP; P01789; LMCP.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL 1 19				
FT	CHAIN 20 147				
FT	MOD_RES 20 20				
FT	DISULFID 41 115				
FT	CONFLICT 21 21				
FT	CONFLICT 53 54				
FT	CONFLICT 67 68				
FT	CONFLICT 125 125				
FT	NON_TER 147 147				
SQ	SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;				
Query Match 67.3%; Score 68; DB 1; Length 147;					
Best Local Similarity 58.8%; Pred. No. 0.00083;					
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;					

QY	1 WIDPENGSDYAPKFG 17
	: : :
Db	69 WINPNSGGTNYAPRFQG 85

RESULT 2

```
HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
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CC -----
DR EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVHU35.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 51.5%; Score 52; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.21;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFG 17
I:| :| :| :| :|
Db 70 INPSGGTNYAQKFG 85

RESULT 3
HV1B_HUMAN
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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CC -----
DR EMBL; J00240; AAA52988.1; -
DR PIR; A02024; HVHDHG.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 50.5%; Score 51; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.31;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFG 17
I:| :| :| :| :|
Db 70 INPSGGTNYAQKFG 85

RESULT 4
NUD9_HUMAN
ID NUD9_HUMAN STANDARD; PRT; 350 AA.
AC Q9BW91;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)
DE (Adenosine diphosphoribose pyrophosphatase) (ADPR-PPase) (ADP-ribose
DE phosphohydrolase) (Nucleoside diphosphate-linked moiety X motif 9).
GN NUDT9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21279171; PubMed=11385575;
RA Perraud A.-L., Fleig A., Dunn C.A., Bagley L.A., Launay P.,
RA Schmitz C., Stokes A.J., Zhu Q., Bessman M.J., Penner R., Kinet J.-P.,
RA Scharenberg A.M.;
RT "ADP-ribose gating of the calcium-permeable LTRPC2 channel revealed by
RT Nudix motif homology."
RL Nature 411:595-599(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ADP-ribose + H(2)O = AMP + D-ribose 5-
CC phosphate.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
CC -----
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CC -----
DR EMBL; AY026252; AAK07671.1; -.
DR EMBL; BC000542; AAH00542.1; -.
DR Genew; HGNC:8056; NUDT9.
```

DR MIM; 606022; -
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00893; NUDIX; 1.
KW Hydrolase.
FT DOMAIN 215 237 NUDIX BOX.
SQ SEQUENCE 350 AA; 39125 MW; 2EA5B24B88FB3420 CRC64;

Query Match 50.5%; Score 51; DB 1; Length 350;
Best Local Similarity 46.7%; Pred. No. 1;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKF 15
| ||: :|::|||
Db 110 WADPQISESNFSPKF 124

RESULT 5
SN_HUMAN STANDARD; PRT: 1709 AA.
AC Q9BZ22; Q9H1H6; Q9H1H7; Q9H7L7; Q9GZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sialoadhesin precursor (Sialic acid binding Ig-like lectin-1) (Siglec-1) (CD169 antigen).
DE 1) (CD169 antigen).
GN SN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Hartnell A., Steel J., Turley H., Jones M., Jackson D., Crocker P.R.;
RT "Characterisation of human sialoadhesin (siglec-1), a sialic acid
RT binding receptor expressed on resident and inflammatory macrophage
RT populations.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehtvaslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE OF 733-1709 FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Spleen;
RA Ohara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human

RT spleen.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MACROPHAGE-RESTRICTED ADHESION MOLECULE THAT MEDIATES
CC SIALIC-ACID DEPENDENT BINDING TO CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
CC SOLUBLE (ISOFORM 2).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:18-22(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/985165905_g.htm".
CC -----
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CC EMBL; AF230073; AAK00757.1; -
DR EMBL; AL109804; CAC17543.1; -
DR EMBL; AL109804; CAC17542.1; -
DR EMBL; AK024462; BAB15752.1; -
DR EMBL; AK024459; BAB15749.1; -
DR EMBL; AK024479; BAB15769.1; -
DR HSSP; Q62230; IQFO.
DR Genew; HGNC:11127; SN.
DR MIM; 600751; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 14.
DR SMART; SM00409; IG; 17.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00408; Igc2; 14.
KW Signal; Glycoprotein; Cell adhesion; Immunoglobulin domain; Repeat;
KW Transmembrane; Alternative splicing; Antigen.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 1709 SIALOADHESIN.
FT DOMAIN 20 1641 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1642 1662 POTENTIAL.
FT DOMAIN 1663 1709 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 136 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 153 224 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 255 312 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 339 397 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 426 498 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 524 582 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 617 696 IG-LIKE C2-TYPE DOMAIN 6.
FT DOMAIN 722 781 IG-LIKE C2-TYPE DOMAIN 7.
FT DOMAIN 810 883 IG-LIKE C2-TYPE DOMAIN 8.
FT DOMAIN 909 967 IG-LIKE C2-TYPE DOMAIN 9.
FT DOMAIN 998 1074 IG-LIKE C2-TYPE DOMAIN 10.
FT DOMAIN 1100 1156 IG-LIKE C2-TYPE DOMAIN 11.
FT DOMAIN 1186 1248 IG-LIKE C2-TYPE DOMAIN 12.
FT DOMAIN 1274 1331 IG-LIKE C2-TYPE DOMAIN 13.
FT DOMAIN 1360 1432 IG-LIKE C2-TYPE DOMAIN 14.
FT DOMAIN 1458 1518 IG-LIKE C2-TYPE DOMAIN 15.
FT DOMAIN 1547 1620 IG-LIKE C2-TYPE DOMAIN 16.
FT DISULFID 41 98 BY SIMILARITY.
FT DISULFID 160 217 BY SIMILARITY.
FT DISULFID 262 305 BY SIMILARITY.
FT DISULFID 346 390 BY SIMILARITY.
FT DISULFID 433 491 BY SIMILARITY.
FT DISULFID 531 575 BY SIMILARITY.
FT DISULFID 624 689 BY SIMILARITY.
FT DISULFID 729 774 BY SIMILARITY.
FT DISULFID 817 876 BY SIMILARITY.
FT DISULFID 916 960 BY SIMILARITY.

FT DISULFID 1005 1067 BY SIMILARITY.
FT DISULFID 1107 1149 BY SIMILARITY.
FT DISULFID 1193 1241 BY SIMILARITY.
FT DISULFID 1281 1324 BY SIMILARITY.
FT DISULFID 1367 1425 BY SIMILARITY.
FT DISULFID 1465 1511 BY SIMILARITY.
FT DISULFID 1554 1613 BY SIMILARITY.
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 730 730 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 741 741 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 886 886 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1104 1104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1138 1138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1251 1251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1462 1462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1476 1476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1632 1709 ALHRLHQFOQLLVGLVGLLVGLLLGLGACYTWRRRRVCK.
FT QSMGENSEVMAFQKETTQLIDPDAACTSTCAPPLG ->
FT GEGRGLHLPCHSAQKPSS (IN ISOFORM 2).
FT A -> T (IN REF. 1).
FT A -> V (IN REF. 3; BAB15749/BAB15769).
SQ SEQUENCE 1709 AA; 182624 MW; 587C7CCA0B789A6D CRC64;

Query Match 46.5%; Score 47; DB 1; Length 1709;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 NGDSDYAPKFG 17
:||||:|
Db 456 SGDSHSPRFSG 467

RESULT 6
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -I- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
PROTEIN HAS ALSO BEEN DETERMINED.
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 17
|:| | | : | | | |
Db 51 INPNGGTSYNQKFKG 66

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 17
|:| | | : | | | |
Db 51 INPNGGTSYNQKFKG 66

RESULT 8
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----

DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||:|:|
Db 69 WIYPGDSGSKYNEKFG 85

RESULT 9
HV51_MOUSE STANDARD; PRT; 118 AA.
ID HV51_MOUSE
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; lMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 17
|:|:|:|

Db 51 INPNNGGTSYNQKFKG 66
RESULT 10
PUR4_ARATH STANDARD; PRT; 1387 AA.
ID PUR4_ARATH
AC Q9M8D3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable phosphoribosylformylglycinamide synthase, chloroplast
DE precursor (EC 6.3.5.3) (FGAM synthase) (FGAMS) (Formylglycinamide
DE ribotide amidotransferase) (FGARAT) (Formylglycinamide ribotide
DE synthetase).
GN AT1G74260 OR F1017.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
CC (formamido)-N(1)-(5-phospho-D-ribosyl)acetamide + L-glutamate.
CC -!- PATHWAY: De novo purine biosynthesis; fourth step.
CC -!- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS
CC FAMILY.
CC -!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AC020579; AAG52403.1; -.
DR InterPro; IPR000728; AIRS_related.
DR Pfam; PF00586; AIRS; 1.
DR Pfam; PF02769; AIRS_C; 2.
KW Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase;
KW Chloroplast; Transit peptide.
FT TRANSIT 1 ?
FT CHAIN ? 1387 CHLOROPLAST (POTENTIAL).
FT PROBABLE
FT PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
FT SYNTHASE.
FT NP_BIND 387 398 ATP (POTENTIAL).
FT ACT_SITE 1215 1215 GATASE (BY SIMILARITY).
SQ SEQUENCE 1387 AA; 151778 MW; 65E9920DF83F0E95 CRC64;

Query Match 44.6%; Score 45; DB 1; Length 1387;
Best Local Similarity 64.3%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKF 15
|| || || || ||
Db 448 IDASNGASDYGKFK 461

RESULT 11
MCEL_SCHPO
ID MCEL_SCHPO STANDARD; PRT; 402 AA.
AC P40997;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE mRNA capping enzyme alpha subunit (mRNA guanylyltransferase)
DE (EC 2.7.7.50) (GTP--RNA guanylyltransferase) (Gtase).
GN CEG1 OR PCE1 OR SPBC2F12.08C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=95083638; PubMed=7991582;
RX Shuman S., Liu Y., Schwer B.;
RA "Covalent catalysis in nucleotidyl transfer reactions: essential motifs in Saccharomyces cerevisiae RNA capping enzyme are conserved in Schizosaccharomyces pombe and viral capping enzymes and among polynucleotide ligases.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12046-12050(1994).
RN [2]
SEQUENCE FROM N.A.
RA Fresco L.D., Woo S., Buratowski S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lucas M., Rochet S., Xiangu Z., Hunt C., Moore K., Hurst S.M., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovsky G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: SECOND STEP OF M-RNA CAPPING. TRANSFER OF THE GMP MOIETY OF GTP TO THE 5' END OF RNA YIELDING A 52 kDa ENZYME-GMP COVALENT REACTION INTERMEDIATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: GTP + (5')PP-pur-mRNA - diphosphate + G(5')PPP-pur-mRNA.

CC -!- SUBUNIT: THE M-RNA CAPPING ENZYME IS COMPOSED OF TWO SEPARATE CHAINS ALPHA AND BETA, RESPECTIVELY A MRNA GUANYLYLTRANSFERASE AND AN RNA 5'-TRIPHOSPHATASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC GTASE FAMILY.
CC -----
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CC -----
CC EMBL; U16143; AAA64996.1; -;
DR EMBL; U18811; AAA58715.1; -;
DR EMBL; Z97211; CAB10156.1; -;
DR InterPro; IPR001339; mRNA_cap_enzyme.
DR Pfam; PF01331; mRNA_cap_enzyme; 1.
KW Transferase; Nucleotidyltransferase; mRNA processing; mRNA capping;
KW Nuclear protein.
FT ACT_SITE 67 67 GUANYLYLATION SITE.
FT MUTAGEN 67 67 K->A: LOSS OF FUNCTION.
SQ SEQUENCE 402 AA; 46875 MW; 76B1E2052DABB974 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 402;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 4 PENGSDYA--PKFQ 16
|| || || || ||
Db 260 PEEGDIDYSAMPEFQ 274

RESULT 12
CHS2_NEUCR
ID CHS2_NEUCR STANDARD; PRT; 944 AA.
AC P30589;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Chitin synthase 2 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase 2).
DE CHS-2.
GN Neurospora crassa.
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95039879; Pubmed=7952169;
RA Din A.B., Yarden O.;
RT "The Neurospora crassa chs-2 gene encodes a non-essential chitin synthase.";
RL Microbiology 140:2189-2197(1994).
RN [2]
RP SEQUENCE OF 250-438 FROM N.A.
RX MEDLINE=92115692; Pubmed=1731323;
RA Bowen A.R., Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J., Robbins P.W.;
RT "Classification of fungal chitin synthases.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).
CC -!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
CC -!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}(N) = UDP + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}(N+1).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -!- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
CC -----
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DR EMBL; X77782; CAA54816.1; -.
DR EMBL; M82951; AAA33582.1; -.
DR PIR; B45189; B45189.
DR InterPro; IPR004834; Chitin_synth.
DR Pfam; PF01644; Chitin_synth; 1.
DR ProDom; PD002998; Chitin_synth; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Cell wall;
KW Multigene family.
FT TRANSMEM 597 617 POTENTIAL.
FT TRANSMEM 634 654 POTENTIAL.
FT TRANSMEM 669 689 POTENTIAL.
FT TRANSMEM 713 733 POTENTIAL.
FT TRANSMEM 873 893 POTENTIAL.
SQ SEQUENCE 944 AA; 106816 MW; F70052AEE083060D CRC64;

Query Match 43.6%; Score 44; DB 1; Length 944;
Best Local Similarity 47.1%; Pred. No. 39;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFGQ 17
|| : ||:| ||:|
Db 917 WIXEKWGDADVKGKFEQ 933

RESULT 13
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVMSG7.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 42.6%; Score 43; DB 1; Length 120;
Best Local Similarity 47.1%; Pred. No. 5.8;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFGQ 17
:|:| | : | ||:
Db 49 YINPGNGYTKYNEKFG 65

RESULT 14
YIGB_ECOLI

ID YIGB_ECOLI STANDARD; PRT; 238 AA.
AC P23306; P76757;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yigB.
GN YIGB OR B3812.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RT from 84.5 to 86.5 minutes.";
RL Science 257:771-778(1992).
RN [2]
RP REVISION TO 13.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91072248; PubMed=2254268;
RA Colloms S.D., Sykora P., Szatmari G., Sherratt D.J.;
RT "Recombination at ColeI cer requires the Escherichia coli xerC gene
RT product, a member of the lambda integrase family of site-specific
RT recombinases.";
RL J. Bacteriol. 172:6973-6980(1990).
RN [4]
RP SEQUENCE OF 183-238 FROM N.A.
RX MEDLINE=84272253; PubMed=6379604;
RA Finch P.W., Emmerson P.T.;
RT "The nucleotide sequence of the uvrD gene of E. coli.";
RL Nucleic Acids Res. 12:5789-5799(1984).
RN [5]
RP SEQUENCE OF 183-238 FROM N.A.
RX MEDLINE=84169504; PubMed=6324092;
RA Easton A.M., Kushner S.R.;
RT "Transcription of the uvrD gene of Escherichia coli is controlled by
RT the lexA repressor and by attenuation.";
RL Nucleic Acids Res. 11:8625-8640(1983).
CC -!- SIMILARITY: TO E.COLI YJG.

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DR EMBL; M87049; AAA67608.1; -.
DR EMBL; AE000457; AAC76815.1; -.
DR EMBL; M38257; AAA24764.1; -.
DR EMBL; X00738; -, NOT_ANNOTATED_CDS.
DR PIR; D37841; D37841.
DR PIR; S30702; S30702.
DR EcoGene; EG11202; yigB.
DR InterPro; IPR001454; Hlgnase/hydrase.
DR Pfam; PF00702; Hydrolase; 1.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 13 13 L -> V (IN REF. 1).
FT CONFLICT 200 200 S -> T (IN REF. 3).

SQ SEQUENCE 2238 AA; 27122 MW; 9C1BDE710641E0D6 CRC64;
Query Match 42.6%; Score 43; DB 1; Length 238;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENG D 8
| | | | |
Db 206 WIRPENG D 213

RESULT 15
C772_SOLME STANDARD; PRT; 511 AA.
AC P37124; (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytochrome P450 77A2 (EC 1.14.-.-) (CYPLXXVIIA2) (P-450EG5).
GN CYP77A2 OR: CYPEG5.
OS Solanum melongena (Eggplant) (Aubergine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID: 4111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv1 Sinsadoharanasu; TISSUE=Hypocotyl;
RX MEDLINE=940139942; PubMed=8307197;
RA Toguri T.; Tokugawa K.;
RT "Cloning of eggplant hypocotyl cDNAs encoding cytochromes P450
belonging to a novel family (CYP77).";
RL FEBS Lett. 338:290-294(1994).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
CC EMBL; X71655; CAA50646.1; -.
DR PIR; S41598; S41598.
DR PIR; S40266; S40266.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Heme; Multigene family.
FT BINDING 456 456 HEME (BY SIMILARITY).
SQ SEQUENCE 511 AA; 58114 MW; 4B2A185D4DAFE023 CRC64;

Query Match 42.6%; Score 43; DB 1; Length 511;
Best Local Similarity 43.8%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPRFQ 16
| | | | |
Db 479 WADPENTRVDFTEKLE 494

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 7.05039 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	76	75.2	468	11 Q99L31	Q99L31 mus musculu
2	60	59.4	497	4 Q8WY24	Q8WY24 homo sapien
3	59	58.4	614	4 Q96GA6	Q96GA6 homo sapien
4	58	57.4	109	11 Q9JL85	Q9JL85 mus musculu
5	57.5	56.9	150	4 Q9Y298	Q9Y298 homo sapien
6	56	55.4	125	4 Q9UL95	Q9UL95 homo sapien
7	55	54.5	119	4 Q9UL94	Q9UL94 homo sapien
8	54	53.5	481	11 Q8VCV5	Q8VCV5 mus musculu
9	51	50.5	124	4 Q9UL92	Q9UL92 homo sapien
10	51	50.5	300	11 Q9D0U2	Q9D0U2 mus musculu
11	51	50.5	350	4 Q96KB3	Q96KB3 homo sapien
12	50	49.5	500	4 Q9BRV0	Q9BRV0 homo sapien
13	48.5	48.0	474	11 Q8R3H6	Q8R3H6 mus musculu
14	48	47.5	102	11 Q9JL79	Q9JL79 mus musculu
15	48	47.5	147	11 Q925S3	Q925S3 mus musculu
16	48	47.5	323	10 Q9STS2	Q9STS2 arabidopsis

17	48	47.5	379	10 Q8RYD8	Q8ryd8 arabidopsis
18	48	47.5	403	16 Q8YLU7	Q8ylu7 ralstonia s
19	48	47.5	484	11 Q99LA6	Q99la6 mus musculu
20	48	47.5	526	17 Q8TJE3	Q8tje3 methanosarc
21	47	46.5	481	11 Q91WT1	Q91wt1 mus musculu
22	47	46.5	520	11 Q92LT2	Q92lt2 mus musculu
23	46	45.5	117	11 Q9QXF0	Q9qxf0 mus musculu
24	46	45.5	117	11 Q9QXE9	Q9qxe9 mus musculu
25	46	45.5	159	4 Q96QS0	Q96qs0 homo sapien
26	46	45.5	1737	11 Q9JIO4	Q9ji04 rattus norv
27	45.5	45.0	118	11 Q9ZLC4	Q9zlc4 mus musculu
28	45	44.6	138	2 Q9F8N0	Q9f8n0 carboxydoth
29	45	44.6	168	17 Q27394	Q27394 methanobact
30	45	44.6	179	10 Q9XI82	Q9xi82 arabidopsis
31	45	44.6	318	10 Q9LMF3	Q9lmf3 arabidopsis
32	45	44.6	348	5 O16334	O16334 caenorhabdi
33	45	44.6	1289	10 Q8VYU2	Q8vyu2 vigna ungui
34	44.5	44.1	462	16 Q8YU74	Q8y074 ralstonia s
35	44	43.6	219	16 O34915	O34915 bacillus su
36	44	43.6	224	9 O64131	O64131 bacteriopha
37	44	43.6	224	16 O31916	O31916 bacillus su
38	44	43.6	234	10 Q9STK0	Q9stk0 arabidopsis
39	44	43.6	238	10 Q93WL3	Q93wl3 arabidopsis
40	44	43.6	249	16 O69834	O69834 streptomyce
41	44	43.6	317	17 Q9YD93	Q9yd93 aeropyrum p
42	44	43.6	387	10 Q9SHD8	Q9shd8 arabidopsis
43	44	43.6	392	10 Q9SLA1	Q9sla1 arabidopsis
44	44	43.6	488	11 Q91WR1	Q91wr1 mus musculu
45	44	43.6	687	10 Q9LHA3	Q9lha3 arabidopsis

ALIGNMENTS

RESULT 1

Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Similar to RIKEN cdna 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 75.2%; Score 76; DB 11; Length 468;
Best Local Similarity 75.0%; Pred. No. 0.00095;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 16
|||||:|:|
Db 69 WIDPEDGETKYAPKFG 84

FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 56.9%; Score 57.5; DB 4; Length 150;
Best Local Similarity 55.0%; Pred. No. 0.21;
Matches 11; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 WI---DPENGSDSYAPKFG 17
|: |||:|:|:|:|
Db 66 WVGFDPESGESIYAREFG 85

RESULT 6
Q9UL95
ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 125
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 55.4%; Score 56; DB 4; Length 125;
Best Local Similarity 52.9%; Pred. No. 0.29;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17
||:|:|:|:|:|
Db 50 WINPNSGGTNYAQKVG 66

RESULT 7
Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 119
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 54.5%; Score 55; DB 4; Length 119;
Best Local Similarity 52.9%; Pred. No. 0.4;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17
||:|:|:|:|:|
Db 50 WINPNSWTTNYAQKFG 66

RESULT 8
Q8VCV5
ID Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC018455; AAH18455.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 53.5%; Score 54; DB 11; Length 481;
Best Local Similarity 58.8%; Pred. No. 3;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17
:||| || | | ||:|
Db 69 YIDPYNGGSSYNQKFKG 85

RESULT 9
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
Query Match 49.5%; Score 50; DB 4; Length 500;
Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
||| : : : ||||
Db 69 WISPSSDNTFRKKFG 85
RESULT 13
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
Query Match 48.0%; Score 48.5; DB 11; Length 474;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 10; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
QY 1 WID--PENGSDYAPKFG 17
||| :||: ||||
Db 66 WIGRIFFGDGTHSGKFG 85
RESULT 14
Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin";
RT Infect. Immun. 68:5803-5808(2000).
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206027; AAF69325.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 47.5%; Score 48; DB 11; Length 102;
Best Local Similarity 47.1%; Pred. No. 4.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
||| :||: ||||
Db 35 WINTETGEPTYADDFKG 51
RESULT 15
Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain";
RT Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
Query Match 47.5%; Score 48; DB 11; Length 147;
Best Local Similarity 47.1%; Pred. No. 6.6;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
||| :||: ||||
Db 52 WIFPGEGSTYNEKFKG 68
Search completed: December 23, 2002, 07:29:58
Job time : 9.05039 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 21.0872 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-22
Perfect score: 631
Sequence: 1 QVKLQSGAELVSGASVKL.....AAYGDYEGYWGQGTVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	558.5	88.5	535	4	US-08-983-035A-38
2	536.5	85.0	118	3	US-08-767-128-22
3	517.5	82.0	270	2	US-08-652-507-2
4	511.5	81.1	124	1	US-08-017-570-6
5	511.5	81.1	124	1	US-08-471-426-6
6	511.5	81.1	124	5	PCT-US94-01709-6
7	511.5	81.1	553	2	US-08-661-052-16
8	511.5	81.1	553	4	US-09-188-082-16
9	511.5	81.1	553	4	US-09-364-088-16
10	511.5	81.1	553	4	US-09-102-716-16
11	506.5	80.3	124	1	US-08-017-570-4
12	506.5	80.3	124	1	US-08-471-426-4
13	506.5	80.3	124	5	PCT-US94-01709-4
14	503.5	79.8	124	4	US-09-672-609-1
15	503.5	79.8	124	4	US-09-025-403A-1
16	502.5	79.6	281	4	US-09-423-439-44
17	502.5	79.6	642	4	US-09-423-439-26
18	502.5	79.2	666	4	US-09-423-439-51
19	499.5	79.2	255	4	US-09-171-945-19
20	484.5	76.8	120	4	US-09-171-945-11
21	481.5	76.3	136	4	US-08-348-548-8
22	481.5	76.3	136	5	PCT-US95-15716-8
23	481	76.2	125	2	US-08-561-521-44
24	481	76.2	125	5	PCT-US95-01219-44
25	478	75.8	117	2	US-08-290-592E-18
26	478	75.8	117	5	PCT-US95-10053-15
27	478	75.8	117	5	PCT-US96-09448-18

28	476	75.4	136	4	US-08-646-265A-29	Sequence 29, Appl
29	471.5	74.7	118	2	US-08-232-081B-38	Sequence 38, Appl
30	469	74.3	123	2	US-08-561-521-9	Sequence 9, Appl
31	469	74.3	123	5	PCT-US95-01219-9	Sequence 9, Appl
32	467	74.0	121	2	US-08-822-830B-13	Sequence 13, Appl
33	464	73.5	121	2	US-08-822-830B-2	Sequence 2, Appl
34	462	73.2	120	2	US-08-950-660-2	Sequence 2, Appl
35	462	73.2	120	5	PCT-US93-00030-2	Sequence 2, Appl
36	462	73.2	120	5	PCT-US93-00924-2	Sequence 2, Appl
37	461	73.1	140	2	US-08-561-521-4	Sequence 4, Appl
38	461	73.1	140	5	PCT-US95-01219-4	Sequence 4, Appl
39	459	72.7	136	1	US-08-024-253-2	Sequence 2, Appl
40	456	72.3	254	2	US-08-792-824-4	Sequence 4, Appl
41	456	72.3	254	2	US-08-792-824-7	Sequence 7, Appl
42	456	72.3	254	2	US-08-792-824-10	Sequence 10, Appl
43	456	72.3	254	2	US-08-792-824-13	Sequence 13, Appl
44	451.5	71.6	120	4	US-08-871-488A-15	Sequence 15, Appl
45	448.5	71.1	113	1	US-08-207-169A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-983-035A-38
; Sequence 38, Application US/08983035A
; Patent No. 6326464
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983.035A
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01111
; FILING DATE: 17-JUL-1996
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Strauss, William L.
; REGISTRATION NUMBER: 47,114
; REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

Query Match 88.5%; Score 558.5; DB 4; Length 535;
Best Local Similarity 88.9%; Pred. No. 6.5e-49;


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; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-017-570-6

Query Match      81.1%; Score 511.5; DB 1; Length 124
Best Local Similarity 77.2%; Pred. No. 6.7e-45;
Matches 98; Conservative 9; Mismatches 7; Indels 1

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPEN
Db 1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYIMHWVKQRPEQGLEWIGWIDPEN

QY 61 APKFQ GKATMTADSSNTAYLQLSLTSEDFAVYVCNA-----YYGDYEG
Db 61 APKFQ GKATMTTDTSSNTAYLQLSLTSEDFAVYCNTRGLSTMITTRWFFD---

QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 5
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O.Box 1967
;

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; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-426-6

Query Match      81.1%; Score 511.5; DB 1;
Best Local Similarity 77.2%; Pred. No. 6.7e-45;
Matches 98; Conservative 9; Mismatches 7;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKQRPEQG
Db 1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVVKQRPEQG
QY 61 APKFQ GKATMTADSSNTAYLQLSLTSED TAVYYCNA-----
Db 61 APKFQ GKATMTDTSSNTAYLQLSLTSED TAVYYCNRGLSTMT
QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 6
PCT-US94-01709-6
; Sequence 6, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOGENIC ANTIBODIES
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

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; NAME: UMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-01709-6

Query Match      81.1%; Score 511.5; DB 5; Length 124;
Best Local Similarity 77.2%; Pred. No. 6.7e-45;
Matches 98; Conservative 9; Mismatches 7; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVVKORPEQGLEWIGWIDPENGDT 60

QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDTAIVYCN-----YYGDYEGYWGQ 110
Db 61 APKFGKATMTDTSSNTAYLQLSSLTSEDTAIVYCNTRGLSTMITTRWFFD---V 117

QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 7
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-661-052-16

Query Match      81.1%; Score 511.5; DB 2; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGSDYA 61
Db 278 IKLQSGAELVRSCTSVKLSCTASGFNIKDSYMHVVKORPEQGLEWIGWIDPEN 337

QY 62 PKFGKATMTADSSSNTAYLQLSSLTSEDTAIVYCN-----AAYGDYEGYWG 115
Db 338 PKFGKATFTDTSSNTAYLQLSSLTSEDTAIVYCNEGTPTGPYYFD---YWG 394

QY 116 SS 117
Db 395 SS 396

RESULT 8
US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-16

Query Match      81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGSDYA 61
Db 278 IKLQSGAELVRSCTSVKLSCTASGFNIKDSYMHVVKORPEQGLEWIGWIDPEN 337

QY 62 PKFGKATMTADSSSNTAYLQLSSLTSEDTAIVYCN-----AAYGDYEGYWG 115

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Db 338 PKFGKATFTTSSNTAYLQLSSLTSEDTAAYYCNEGTPGYYFD---YWGQTTTV 394
QY 116 SS 117
Db 395 SS 396
RESULT 9
US-09-364-088-16
; Sequence 16, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-16
Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;
QY 2 VKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSYA 61
Db 278 IKLQSGAELVRSVGSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDT EYA 337
QY 62 PKFGKATMTADSSSNTAYLQLSSLTSEDTAAYYCN-----AAYGDYEGYWGQTTTV 115
Db 338 PKFGKATFTTDTSSNTAYLQLSSLTSEDTAAYYCNEGTPGYYFD---YWGQTTTV 394
QY 116 SS 117
Db 395 SS 396
RESULT 10
US-09-102-716-16
; Sequence 16, Application US/09102716

; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16
Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;
QY 2 VKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSYA 61
Db 278 IKLQSGAELVRSVGSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDT EYA 337
QY 62 PKFGKATMTADSSSNTAYLQLSSLTSEDTAAYYCN-----AAYGDYEGYWGQTTTV 115
Db 338 PKFGKATFTTDTSSNTAYLQLSSLTSEDTAAYYCNEGTPGYYFD---YWGQTTTV 394
QY 116 SS 117
Db 395 SS 396
RESULT 11
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 10.8837 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-22
Perfect score: 631
Sequence: 1 QVKLQSGAELVSGASVKL.....AAYGDYEGYWGQGTTVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	117	10	US-09-976-787-23
2	631	100.0	117	10	US-09-865-198-22
3	631	100.0	238	10	US-09-976-787-29
4	631	100.0	238	10	US-09-865-198-28
5	624	98.9	117	10	US-09-976-787-7
6	624	98.9	117	10	US-09-865-198-7
7	624	98.9	240	10	US-09-976-787-28
8	624	98.9	240	10	US-09-865-198-27
9	503.5	79.8	124	9	US-09-974-052-1
10	503.5	79.8	124	9	US-09-974-051-1
11	502.5	79.6	120	10	US-09-910-059-11
12	502.5	79.6	255	10	US-09-910-059-19
13	488.5	77.4	136	10	US-09-564-329A-11
14	488.5	77.4	136	10	US-09-855-153-11
15	488.5	77.4	136	10	US-09-854-811-11
16	488.5	77.4	136	10	US-09-934-773-11
17	488.5	77.4	136	10	US-09-963-620-11
18	478	75.8	117	10	US-09-158-120A-18
19	428.5	67.9	139	10	US-09-809-739-5

20	428	67.8	117	10	US-09-158-120A-17	Sequence 17, Appl
21	422.5	67.0	244	10	US-09-940-391-1	Sequence 1, Appli
22	417.5	66.2	124	9	US-09-974-052-9	Sequence 9, Appli
23	417.5	66.2	124	9	US-09-974-052-12	Sequence 12, Appl
24	417.5	66.2	124	9	US-09-974-051-9	Sequence 9, Appli
25	417.5	66.2	124	9	US-09-974-051-12	Sequence 12, Appl
26	413.5	65.5	124	9	US-09-974-052-8	Sequence 8, Appli
27	413.5	65.5	124	9	US-09-974-051-8	Sequence 8, Appli
28	412.5	65.4	120	10	US-09-910-059-89	Sequence 89, Appl
29	408.5	64.7	120	10	US-09-910-059-79	Sequence 79, Appl
30	407.5	64.6	127	10	US-09-998-831-7	Sequence 7, Appli
31	406.5	64.4	120	10	US-09-910-059-91	Sequence 91, Appl
32	403.5	63.9	120	10	US-09-910-059-85	Sequence 85, Appl
33	402.5	63.8	120	10	US-09-910-059-81	Sequence 81, Appl
34	401.5	63.6	124	9	US-09-974-052-7	Sequence 7, Appli
35	401.5	63.6	124	9	US-09-974-051-7	Sequence 7, Appli
36	401	63.5	138	10	US-09-753-436-78	Sequence 78, Appl
37	400.5	63.5	122	1	US-08-779-784-28	Sequence 28, Appl
38	399.5	63.3	120	10	US-09-910-059-55	Sequence 55, Appl
39	399.5	63.3	153	10	US-09-861-294-4	Sequence 4, Appli
40	399.5	63.3	255	10	US-09-910-059-57	Sequence 57, Appl
41	399.5	63.3	260	10	US-09-910-059-93	Sequence 93, Appl
42	399.5	63.3	306	10	US-09-910-059-95	Sequence 95, Appl
43	399.5	63.3	613	10	US-09-910-059-113	Sequence 113, App
44	399.5	63.3	716	10	US-09-910-059-125	Sequence 125, App
45	398.5	63.2	120	12	US-10-025-687-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match	100.0%;	Score 631;	DB 10;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 1.4e-42;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVKLQSGAELVSGASVKLSCTTSGFNKDFYHMHVVKORPEQGLEWIGWIDPENGDSY	60	
Db	1	QVKLQSGAELVSGASVKLSCTTSGFNKDFYHMHVVKORPEQGLEWIGWIDPENGDSY	60	
QY	61	APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTTVTVSS	117	
Db	61	APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTTVTVSS	117	

RESULT 2
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping

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; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; SOFTWARE: WordPerfect 8.0 for Windows
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match      100.0%; Score 631; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
   |||||

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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RESULT 3
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match      100.0%; Score 631; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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RESULT 4
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
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; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match      100.0%; Score 631; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
   |||||

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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RESULT 5
US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match      98.9%; Score 624; DB 10; Length 117;
Best Local Similarity 99.1%; Pred. No. 4.7e-42;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
   |||||
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60
   |||||

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
   |||||
Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVSS 117
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RESULT 6
US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
```


APPLICANT: Trempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
TITLE OF INVENTION: Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974,051
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/029,694
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 124
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: Murine Col-1 VH
LOCATION: 1..124
US-09-974-051-1

Query Match 79.8%; Score 503.5; DB 9; Length 124;
Best Local Similarity 76.4%; Pred. No. 9.5e-33;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
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Db 1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDT 60
Y 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNA-----YGDYEGYWGQ 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 APKFGKATMTDYSNTAYLQLSSLTSEDYAVYYCNRGLSTMTTRWFFD---VWGAG 117
Y 111 TIVTVSS 117
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Db 118 TIVAVSS 124

RESULT 11
US-09-910-059-11
; Sequence 11, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-11

Query Match 79.6%; Score 502.5; DB 10; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.1e-32;
Matches 97; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 EVQLQSGAELVRSASVKLSCTASGFNIKDNMHVWKORPEQGLEWIAWIDPENGDT 60
Y 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNA--YGDY--EGYWGQTTVT 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 APKFRGKATLTADSSNTAYLHLSSLTSEDYAVYYCHVLIYAGYLAMDYWGQTSVAV 120

RESULT 12

US-09-910-059-19
; Sequence 19, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric HuIgG2 Fd construct
US-09-910-059-19

Query Match 79.6%; Score 502.5; DB 10; Length 255;
Best Local Similarity 80.8%; Pred. No. 2.1e-32;
Matches 97; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 20 EVQLQSGAELVRSASVKLSCTASGFNIKDNMHVWKORPEQGLEWIAWIDPENGDT 79
Y 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNA--YGDY--EGYWGQTTVT 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 80 APKFRGKATLTADSSNTAYLHLSSLTSEDYAVYYCHVLIYAGYLAMDYWGQTSVAV 139

RESULT 13

US-09-564-329A-11
; Sequence 11, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-11

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Query Match	77.4%;	Score 488.5;	DB 10;	Length 136;
Best Local Similarity	77.8%;	Pred. No. 1.5e-31;		
Matches 91;	Conservative	10;	Mismatches 11;	Indels 5; Gaps 1;

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	:	: :	
Dd	14	EVQLQQSGAELVRSGASVKLSCTASGFNIKDYIHWVNQRDPQGLEWIGWIDPENGDTEF	73
Qy	61	APKFQGKATMTADSSNTAYLQLSSLTSEDTAIVYYCNAYYGDEYGWGQTTVTVSS	117
	:	: :	
Dd	74	VPKFQGKATMTADIFSNLAYHLSSLTSEDFAVYYCKT-----GGFWGGTLTVSA	125

RESULT 14
US-09-855-153-11
; Sequence 11, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-11

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Query Match	77.4%;	Score 488.5;	DB 10;	Length 136;
Best Local Similarity	77.8%;	Pred. No. 1.5e-31;		
Matches 91;	Conservative	10;	Mismatches 11;	Indels 5;
				Gaps 1;

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RESULT 15
 US-09-854-811-11
 ; Sequence 11, Application US/09854811
 ; Patent No. US20020119157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/09/854,811
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: 09/564,329
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: SCID Mice
 US-09-854-811-11

Query Match	77.4%;	Score 488.5;	DB 10;	Length 136;
Best Local Similarity	77.8%;	Pred. NO. 1.5e-31;		
Matches 91;	Conservative 10;	Mismatches 11;	Indels 5;	Gaps 1;

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GenCore version 5.1.3
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	403.5	63.9	139	1	HV07_MOUSE	P01751 mus musculu
2	390	61.8	120	1	HV03_MOUSE	P01747 mus musculu
3	385.5	61.1	137	1	HV11_MOUSE	P01755 mus musculu
4	381	60.4	140	1	HV02_MOUSE	P01746 mus musculu
5	377	59.7	117	1	HV12_MOUSE	P01756 mus musculu
6	374	59.3	138	1	HV48_MOUSE	P03980 mus musculu
7	368	58.3	117	1	HV13_MOUSE	P01757 mus musculu
8	368	58.3	136	1	HV15_MOUSE	P01759 mus musculu
9	366.5	58.1	120	1	HV50_MOUSE	P06329 mus musculu
10	364.5	57.8	147	1	HV1C_HUMAN	P01744 homo sapien
11	362.5	57.4	118	1	HV51_MOUSE	P06330 mus musculu
12	348	55.2	121	1	HV01_MOUSE	P01745 mus musculu
13	345	54.7	117	1	HV06_MOUSE	P01750 mus musculu
14	343	54.4	117	1	HV09_MOUSE	P01753 mus musculu
15	339	53.7	117	1	HV04_MOUSE	P01748 mus musculu
16	336	53.2	117	1	HV49_MOUSE	P06328 mus musculu
17	332	52.6	117	1	HV10_MOUSE	P01754 mus musculu
18	332	52.6	117	1	HV52_MOUSE	P06327 mus musculu
19	327	51.8	117	1	HV1B_HUMAN	P01743 homo sapien
20	325	51.5	117	1	HV05_MOUSE	P01749 mus musculu
21	323.5	51.3	119	1	HV40_MOUSE	P01810 mus musculu
22	321.5	51.0	119	1	HV37_MOUSE	P01807 mus musculu
23	320	50.7	117	1	HV14_MOUSE	P01758 mus musculu
24	316.5	50.2	114	1	HV00_MOUSE	P01741 mus musculu
25	314.5	49.8	119	1	HV38_MOUSE	P01808 mus musculu
26	312	49.4	117	1	HV42_MOUSE	P01812 mus musculu
27	309	49.0	117	1	HV1C_HUMAN	P23083 homo sapien
28	308.5	48.9	136	1	HV16_MOUSE	P01783 mus musculu
29	307.5	48.7	122	1	HV3C_HUMAN	P01768 homo sapien
30	305	48.3	142	1	HV01_RAT	P01805 rattus norv
31	303	48.0	117	1	HV1A_HUMAN	P01742 homo sapien
32	296	46.9	118	1	HV39_MOUSE	P01809 mus musculu
33	293.5	46.5	122	1	HV21_MOUSE	P01790 mus musculu

34	293	46.4	117	1	HV41_MOUSE	P01811 mus musculu
35	291	46.1	123	1	HV24_MOUSE	P01793 mus musculu
36	290	46.0	113	1	HV30_MOUSE	P01799 mus musculu
37	290	46.0	115	1	HV32_MOUSE	P01801 mus musculu
38	290	46.0	125	1	HV1F_HUMAN	P06326 homo sapien
39	289	45.8	119	1	HV3L_HUMAN	P01773 homo sapien
40	287	45.5	123	1	HV19_MOUSE	P01788 mus musculu
41	286.5	45.4	116	1	HV3T_HUMAN	P01781 homo sapien
42	286	45.3	113	1	HV31_MOUSE	P01800 mus musculu
43	285	45.2	113	1	HV27_MOUSE	P01796 mus musculu
44	284	45.0	115	1	HV33_MOUSE	P01802 mus musculu
45	283.5	44.9	122	1	HV3A_HUMAN	P01762 homo sapien

ALIGNMENTS

RESULT 1

HV07_MOUSE						
ID	HV07_MOUSE	STANDARD;	PRT;	139	AA.	
AC	P01751; P01752;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Ig heavy chain V region B1-8/186-2 precursor.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6;					
RX	MEDLINE=81234548; PubMed=6788376;					
RA	Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,					
RA	Baltimore D.;					
RT	"Heavy chain variable region contribution to the NPB family of					
RT	antibodies: somatic mutation evident in a gamma 2a variable region.";					
RL	Cell 24:625-637(1981).					
CC	-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA					
CC	MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL					
CC	(NPB ANTIBODIES).					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
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CC	modified and this statement is not removed. Usage by and for commercial					
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to licensee@isb-sib.ch).					
CC	-----					
DR	EMBL; J00529; AAA38170.1; -.					
DR	PIR; A02034; MHMS18.					
DR	HSSP; P01810; 2FBJ.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_v.					
DR	Pfam; PF00047; ig; 1.					
DR	SMART; SM00406; IGV; 1.					
KW	Immunoglobulin V region; Signal.					
KW	SIGNAL 1 19					
FT	CHAIN 20 139					
FT	DOMAIN 20 49					
FT	DOMAIN 50 54					
FT	DOMAIN 55 68					
FT	DOMAIN 69 85					
FT	DOMAIN 86 117					
FT	DOMAIN 118 124					
FT	DOMAIN 125 139					
FT	DISULFID 41 115					
FT	NON_TER 139 139					
SQ	SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;					

Query Match 63.9%; Score 403.5; DB 1; Length 139;
Best Local Similarity 65.8%; Pred. No. 2.4e-33;

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DR	EMBL; J00493; AAA38128.1; -.
DR	PIR; A02028; HVMSG7.
DR	HSSP; P01810; 2FBJ.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; Igv; 1.
DR	Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT	NON_TER 140 140
FT	SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
SQ	


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RESULT 10
HV1C_HUMAN          STANDARD;          PRT;      147 AA.
AC  P01744;
DT  21-JUL-1986 (Rel. 01, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Ig heavy chain V-I region ND precursor (Fragments).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83065234; PubMed=6815656;
RA  Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA  Bell L.O., Gould H.J.;
RT  "Cloning and sequence determination of the gene for the human
RT  immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL  Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN  [2]
RP  SEQUENCE OF 20-147.
RA  Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL  (In) Bach M.K. (eds.);
RL  Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL  Marcel Dekker, New York (1978).
CC  -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC  PROTEIN.
DR  PIR; A02026; ELHUND.
DR  HSSP; P01789; IMCP.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL          1 19
FT  CHAIN           20 147  IG HEAVY CHAIN V-I REGION ND.
FT  MOD_RES        20 20  PYRROLIDONE CARBOXYLIC ACID.
FT  DISULFID       41 115
FT  CONFLICT       21 21  T -> V (IN REF. 2).
FT  CONFLICT       53 54  IH -> HI (IN REF. 2).
FT  CONFLICT       67 68  VG -> GV (IN REF. 2).
FT  CONFLICT      125 125  MISSING (IN REF. 2).
FT  NON_TER       147 147
SQ  SEQUENCE      147 AA; 16491 MW;  948F9F72A5366C20 CRC64;

Query Match          57.8%; Score 364.5; DB 1; Length 147;
Best Local Similarity 51.6%; Pred. No. 1.9e-29;
Matches 66; Conservative 25; Mismatches 26; Indels 11; Gaps 2;

QY  1 QVKLQSGAELVGSGAVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
   I : I I I I I : I I I I I I I I I : I I I I I I I I I : I : I
Db  20 QTQLVQSGAEVRKPGASVRVCKASGYTFIDSYIHWRQAPGHGLEWVGWINPSGGTNY 79

QY  61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYYC---NAYYGDYEGY-----WGQ 109
   I I I I I : I I I I I : I I I I I I I I I : : I I :
Db  80 APRFQGRVTMTDRDASFSTAYMDLRLSLRSDDSAVFYCAKSDPFWSDYINFDSYTLDDVWGQ 139

QY  110 GTTVTVSS 117
   I I I I I I I
Db  140 GTTVTVSS 147

RESULT 11
HV51_MOUSE
ID  HV51_MOUSE          STANDARD;          PRT;      118 AA.
AC  P06330;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-JAN-1988 (Rel. 06, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region AC38 205.12.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=84182519; PubMed=6201362;
RA  Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT  "A V region determinant (idiotope) expressed at high frequency in B
RT  lymphocytes is encoded by a large set of antibody structural genes.";
RL  EMBO J. 3:517-523(1984).
DR  PIR; A02040; MHMS38.
DR  HSSP; P01789; IMCP.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region.
FT  DOMAIN         1 98  V SEGMENT.
FT  DOMAIN         99 104  D SEGMENT.
FT  DOMAIN        105 118  J SEGMENT.
FT  DISULFID       22 96  BY SIMILARITY.
FT  NON_TER       118 118
SQ  SEQUENCE      118 AA; 12934 MW;  94F7BEE4C762A018 CRC64;

Query Match          57.4%; Score 362.5; DB 1; Length 118;
Best Local Similarity 59.7%; Pred. No. 2.3e-29;
Matches 71; Conservative 17; Mismatches 28; Indels 3; Gaps 2;

QY  1 QVKLQSGAELVGSGAVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
   : I I I I I I I I I I I I I I I : I I I I I I I I I : I I I : I
Db  1 EVQLQSGPELVKPGASVKISKASGYTFTDYIMNWKQSHGKSLEWIGDINPNNGTSY 60

QY  61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYYCNAVYGDYEGY--WGQTTTVTVSS 117
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db  61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARGYG-YDPFDVWGTTTVTVSS 118

RESULT 12
HV01_MOUSE
ID  HV01_MOUSE          STANDARD;          PRT;      121 AA.
AC  P01745;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region MPC 11.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81053741; PubMed=6253904;
RA  Zakut R., Cohen J., Givol D.;
RT  "Cloning and sequence of the cDNA corresponding to the variable
RT  region of immunoglobulin heavy chain MPC11.";
RL  Nucleic Acids Res. 8:3591-3601(1980).
RN  [2]
RP  REVISIONS.
RA  Zakut R., Cohen J., Givol D.;
RL  Nucleic Acids Res. 8:4839-4840(1980).
CC  -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC  FROM A MYELOMA THAT SECRETES IGG2B.
DR  PIR; A02027; GVMS11.
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region.
FT  NON_TER       121 121
SQ  SEQUENCE      121 AA; 13135 MW;  227AEF3EC56ED0BF CRC64;

Query Match          55.2%; Score 348; DB 1; Length 121;
Best Local Similarity 56.2%; Pred. No. 6.6e-28;
```



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DR PIR; A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 53.7%; Score 339; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 4.9e-27;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
   ||||| ||| ||||||| ||: :||||||| ||||||| |:| || :|
Db 20 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNINPGNGGTNY 79

QY 61 APKFQGKATMTADSSNTAYLQLSLTSEDYAVYYC 96
   ||: ||: ||: ||| |||||||: ||||
Db 80 NEKFKSKVTLTVDKSSSTAYTQLSLTSEDSAVYYC 115
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Search completed: December 23, 2002, 07:26:13
Job time : 11.564 secs

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QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVVYC--NAYYGDYEGYWGQGTTVTVSS 117
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 80 APKFDKATITADTSSNTAYLQLSSLTSEDYAVVYCARNLLYGGYDYWGQGTITVSS 138
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
RESULT 2
Q9JL85
ID Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin-heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;
Query Match 67.8%; Score 428; DB 11; Length 109;
Best Local Similarity 77.1%; Pred. No. 7e-37;
Matches 84; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
QY 9 AELVGGASVKLSCTTSGFNKDFYMHVVKQRPQGLEWIDPENGSDYAPKFGCKA 68
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 1 AELVKPGASVKLSCTASGFNIEDTYMHVVKQRPQGLEWIGRIDPATGHSKYDPKFGCKA 60
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
QY 69 TMTADSSNTAYLQLSSLTSEDYAVVYCNAAYYGDYEGYWGQGTTVTVSS 117
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 61 TMTDSSNTAYLQLSSLTSEDYAVVYCVRRGAVVFDYWGQGTALTAVSS 109
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
RESULT 3
Q924P9
ID Q924P9 PRELIMINARY; PRT; 143 AA.
AC Q924P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
GN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069916; BAB63932.1; -.
DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;
Query Match 65.2%; Score 411.5; DB 11; Length 143;
Best Local Similarity 66.9%; Pred. No. 5e-35;
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;
QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKQRPQGLEWIDPENGSDY 60
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 1 QVQLQQGAEELVPGASVKLSCKASGYTFTSYMQWQVQKRPQGLEWIGIDPNSGTY 60
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVVYC-NAYYGDYEGYWGQGTTVTVSS 117
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 61 NQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCASHYVSSSDYWGQGTTLTVSS 118
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
RESULT 4
Q924R8
ID Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;
Query Match 64.5%; Score 407; DB 11; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.5e-34;
Matches 79; Conservative 14; Mismatches 24; Indels 4; Gaps 2;
QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKQRPQGLEWIDPENGSDY 60
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 1 QVQLQQPQAEELVPGASVKLSCKASGYTFTSYMHVVKQRPGRGLEWIGRIDPNSGGTKY 60
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVVYC-NAYYGD--YEGYWGQGTTVTVSS 116
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCARSYYGSSLYYFDYWGQGTTLTVSS 120
||||| :|||:|||||:|||||:|||||:||||| :||| :|||||:|||||
QY 117 S 117
Db 121 S 121
RESULT 5
Q924Q7
ID Q924Q7 PRELIMINARY; PRT; 145 AA.
AC Q924Q7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AB067793; BAB63278.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 63.9%; Score 403.5; DB 11; Length 145;
Best Local Similarity 65.8%; Pred. No. 3.4e-34;
Matches 79; Conservative 13; Mismatches 25; Indels 3; Gaps 2;

QY 1 QVKLQQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGWIDPENGDSY 60
Db 1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKRPGRGLEWIGRIDPNSSGTTY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYYCNA--YYG-DYEGYWGQGTITVTVSS 117
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYGYSSYFDYWGQGTITVTVSS 120

RESULT 6
Q924Q3 PRELIMINARY; PRT; 146 AA.
ID Q924Q3
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AB067797; BAB63282.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 146
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 63.9%; Score 403; DB 11; Length 146;
Best Local Similarity 66.1%; Pred. No. 3.9e-34;
Matches 80; Conservative 14; Mismatches 23; Indels 4; Gaps 3;

QY 1 QVKLQQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGWIDPENGDSY 60
Db 1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKRPGRGLEWIGRIDPNSSGTTY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYYC--NAY-YGDYE-GYWGQGTITVTVS 116
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSLYDYGDIAMDYWGQGTITVTVS 120

QY 117 S 117
Db 121 S 121
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```
RESULT 7
Q9Z1C4 PRELIMINARY; PRT; 118 AA.
ID Q9Z1C4
AC Q9Z1C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 63.5%; Score 400.5; DB 11; Length 118;
Best Local Similarity 66.1%; Pred. No. 5.5e-34;
Matches 78; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

QY 1 QVKLQQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGWIDPENGDSY 60
Db 1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKORPGQGLEWIGAIYPGCGDTSY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYYC-NAYYGDYEGYWGQGTITVTVSS 117
Db 61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARTVGGYFDYWGQGTITVTVSS 118

RESULT 8
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060O09 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
Query Match 63.5%; Score 400.5; DB 11; Length 473;
Best Local Similarity 63.7%; Pred. No. 3e-33;
Matches 79; Conservative 16; Mismatches 22; Indels 7; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 QVQLQSDAELVKGASVKISCKVSGYTFDHTIHVWKORPEQGLEWIGYIYPRDGSTKY 79
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYVC---NAYYG---DYEGYWGQTTV 113
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGSIYGYGLYFDYWGQTTI 139
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 114 TVSS 117
  |||||
Db 140 TVSS 143
  |||||

RESULT 9
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR.1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann J., Mashima J., Lee N.H.,
RA Lyons P., Marchionni L., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Query Match 63.2%; Score 399; DB 11; Length 473;

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Best Local Similarity 64.7%; Pred. No. 4.3e-33;
Matches 77; Conservative 18; Mismatches 22; Indels 2; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 QVQLQSGAELVKGASVKISCKASGYTFDYYINWVKORPGQGLEWIGKIGPGSGSTYY 79
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYVC---NAYGDYEGYWGQTTVTSS 117
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVYFCARSGYDYDFWYWGQTLTVSA 138
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
Q924R0
ID Q924R0 PRELIMINARY; PRT; 143 AA.
AC Q924R0;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067790; BAB63275.1; -.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00408; IGC2; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 63.2%; Score 398.5; DB 11; Length 143;
Best Local Similarity 65.3%; Pred. No. 1.1e-33;
Matches 77; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLQPGAELVKGASVKLSCKASGYTFTSYWMHWKORPGGLEWIGRIDPNSSGGTKY 60
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYVCNAYYGDYE-GYWGQTTVTSS 117
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYFCARWDEYAMDYWGQTSVTSS 118
  ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
Q924Q5
ID Q924Q5 PRELIMINARY; PRT; 143 AA.
AC Q924Q5;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
```

RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB067795; BAB63280.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 143
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match 63.2%; Score 398.5; DB 11; Length 143;
Best Local Similarity 65.5%; Pred. No. 1.1e-33;
Matches 78; Conservative 14; Mismatches 24; Indels 3; Gaps 2;

QY 1 QVKLQSQGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
||:||||| ||||| ||: ::||| ||| :||| ||| :| :|
Db 1 QVQLQOPGAELVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGY--WGQGT VTVVSS 117
||: |||:| | :|||:|||||:|||| :| ||| : || |||||
Db 61 NEKF KSKATLTVDKPSSTAYMQLSSLTSEDSAVYICARFY-DYEYFDVWGCTGT VTVVSS 118

RESULT 12
Q924R2
ID Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB067788; BAB63273.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 140
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 63.1%; Score 398; DB 11; Length 140;
Best Local Similarity 66.1%; Pred. No. 1.2e-33;
Matches 78; Conservative 13; Mismatches 23; Indels 4; Gaps 2;

QY 1 QVKLQSQGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
||:||||| ||||| ||: ::||| ||| :||| ||| :| :|
Db 1 QVQLQOPGAELVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGT VTVVSS 117
||: |||:| | :|||:|||||:|||| :| ||| : || |||||
Db 61 NEKF KSKATLTVDKPSSTAYMQLSSLTSEDSAVYICARIYAGD---YWGQGT VTVVSS 115

RESULT 13
Q924Q1
ID Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB069913; BAB63929.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 142
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 62.9%; Score 397; DB 11; Length 142;
Best Local Similarity 65.0%; Pred. No. 1.6e-33;
Matches 76; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 QVKLQSQGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
||:||||| ||||| ||: ::||| ||| :||| ||| :| :|
Db 1 QVQLQOPGTTELKPGASVKLSCKASGYTFTSYNMHWVKQRPQGLEWIGNPNSGGTNY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGT VTVVSS 117
||: |||:| | :|||:|||||:|||| :| ||| : || |||||
Db 61 NEKF KSKATLTVDKSSSTAYMQLSSLTSEDSAVYICARRGWEAMDYWGQGT VTVVSS 117

RESULT 14
Q924R4
ID Q924R4 PRELIMINARY; PRT; 145 AA.
AC Q924R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB067785; BAB63270.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 145
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16081 MW; ECDB1A135E05B8AA CRC64;

Query Match 62.7%; Score 395.5; DB 11; Length 145;
Best Local Similarity 64.2%; Pred. No. 2.3e-33;
Matches 77; Conservative 14; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVKLQSQGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
||:||||| ||||| ||: ::||| ||| :||| ||| :| :|
Db 1 QVQLQOPGAELVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYE--GYWGQGT VTVVSS 117
||: |||:| | :|||:|||||:|||| :| ||| : || |||||
Db 61 NEKF KSKATLTVDKPSSTAYMQLSSLTSEDSAVYICARSDYDYDYAMDYWGQGT VTVVSS 120

RESULT 15
Q924R1
ID Q924R1 PRELIMINARY; PRT; 145 AA.

Search completed: December 23, 2002, 07:29:59
Job time : 49:5233 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 19.1047 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-23
Perfect score: 549
Sequence: 1 DIELTQSPAIMASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	534	97.3	235	4	US-09-171-945-17
2	532	96.9	108	4	US-09-171-945-9
3	529	96.4	129	2	US-08-116-778E-2
4	529	96.4	129	2	US-08-438-562-2
5	529	96.4	129	2	US-08-483-528B-92
6	523	95.3	270	2	US-08-652-507-2
7	523	95.3	553	2	US-08-661-052-16
8	523	95.3	553	4	US-09-188-082-16
9	523	95.3	553	4	US-09-364-088-16
10	523	95.3	553	4	US-09-102-716-16
11	521	94.9	281	4	US-09-423-439-44
12	521	94.9	666	4	US-09-423-439-51
13	518	94.4	105	3	US-08-434-000A-12
14	518	94.4	105	4	US-09-312-157-12
15	516	94.0	106	1	US-07-634-278-1
16	516	94.0	106	1	US-07-634-278-16
17	516	94.0	106	1	US-08-477-728-1
18	516	94.0	106	1	US-08-477-728-16
19	516	94.0	106	1	US-08-474-040-1
20	516	94.0	106	1	US-08-474-040-16
21	516	94.0	106	1	US-08-487-200-1
22	516	94.0	106	1	US-08-487-200-16
23	516	94.0	106	1	US-08-488-113B-163
24	516	94.0	106	1	US-08-477-484B-163
25	516	94.0	106	1	US-08-107-669D-49
26	516	94.0	106	1	US-08-472-788A-83
27	516	94.0	106	2	US-08-477-531B-49

28	516	94.0	106	2	US-08-646-360-163	Sequence 163, Appl
29	516	94.0	106	2	US-08-082-842A-83	Sequence 83, Appl
30	516	94.0	106	4	US-08-839-765-163	Sequence 163, App
31	516	94.0	106	4	US-09-136-389-163	Sequence 163, App
32	516	94.0	106	4	US-08-484-537-1	Sequence 1, Appli
33	516	94.0	106	4	US-08-484-537-16	Sequence 16, Appl
34	516	94.0	106	4	US-09-610-838-163	Sequence 163, App
35	516	94.0	239	3	US-08-279-772A-8	Sequence 8, Appli
36	516	94.0	239	4	US-08-902-486-11	Sequence 11, Appl
37	516	94.0	599	1	US-08-463-163-3	Sequence 3, Appli
38	493	89.8	130	4	US-09-393-385B-113	Sequence 113, App
39	490	89.3	130	4	US-09-393-385B-111	Sequence 111, App
40	489	89.1	128	4	US-08-619-491-2	Sequence 2, Appli
41	489	89.1	128	5	PCT-US95-07302-2	Sequence 2, Appli
42	483	88.0	244	2	US-08-553-497A-20	Sequence 20, Appl
43	481	87.6	107	1	US-08-211-202-3	Sequence 3, Appli
44	481	87.6	246	1	US-08-469-486-57	Sequence 57, Appl
45	481	87.6	246	2	US-08-469-658-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-171-945-17
; Sequence 17, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-17

Query Match	97.3%	Score 534;	DB 4;	Length 235;
Best Local Similarity	96.2%	Pred. No. 1.7e-40;		
Matches 102;	Conservative	3;	Mismatches	1; Indels 0; Gaps 0;
Qy	1	DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR	60	
Db	23	DIELTQSPAIMASPGKVTITCSASSSVTYMHWFQKPGTSPKLIWYSTNLASGVPAR	82	
Qy	61	FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK	106	
Db	83	FSGSGSGTSYSLTISRMEADAATYYCQQRSTYPLTFGAGTKLEIK	128	

RESULT 2
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek


```
;
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
;
; TITLE OF INVENTION:
;
; NUMBER OF SEQUENCES: 8
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 587691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-652-507-2
;
; Query Match 95.3%; Score 523; DB 2; Length 270;
; Best Local Similarity 97.1%; Pred. No. 1.9e-39;
; Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
; QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPARFSG 63
; |||||
; Db 165 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPARFSG 224
; |||||
;
; QY 64 SSGTSYSLTISRMEADAATYQCQRSSYPFTFGSGTKLEIK 106
; |||||
; Db 225 SSGTSYSLTISRMEADAATYQCQRSSYPFTFGSGTKLEIK 267
; |||||
;
; RESULT 7
; US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
;
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
;
; NUMBER OF SEQUENCES: 16
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
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;
; FILING DATE:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-661-052-16
;
; Query Match 95.3%; Score 523; DB 2; Length 553;
; Best Local Similarity 97.1%; Pred. No. 4e-39;
; Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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; QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPARFSG 63
; |||||
; Db 415 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPARFSG 474
; |||||
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; QY 64 SSGTSYSLTISRMEADAATYQCQRSSYPFTFGSGTKLEIK 106
; |||||
; Db 475 SSGTSYSLTISRMEADAATYQCQRSSYPFTFGSGTKLEIK 517
; |||||
;
; RESULT 8
; US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
;
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
;
; NUMBER OF SEQUENCES: 16
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
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; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
;
US-09-423-439-44

Query Match          94.9%; Score 521; DB 4; Length 281;
Best Local Similarity 95.2%; Pred. No. 2.9e-39;
Matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPARF 61
Db 159 IVLTQSPAIMASPGKVTITCSASSSVTYMHWFQOKPGTSPKLIYSTSNLASGVPARF 218

QY 62 SGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
Db 219 SGSGSGTSYSLTISRMEADAATYYCQORSTYPLTFGAGTKLEIK 263

RESULT 12
US-09-423-439-51
; Sequence 51, Application US/09423439
; Patent No. 6339070
;
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
;
US-09-423-439-51

Query Match          94.9%; Score 521; DB 4; Length 666;
Best Local Similarity 95.2%; Pred. No. 7.4e-39;
Matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPARF 61
Db 156 IVLTQSPAIMASPGKVTITCSASSSVTYMHWFQOKPGTSPKLIYSTSNLASGVPARF 215

QY 62 SGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
Db 216 SGSGSGTSYSLTISRMEADAATYYCQORSTYPLTFGAGTKLEIK 260

RESULT 13
US-08-434-000A-12
; Sequence 12, Application US/08434000A
; Patent No. 6046037
;
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; PRIOR APPLICATION DATA: 08/367,395
; APPLICATION NUMBER: 12/30/94
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; TELEX: SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; TOPOLOGY: DESCRIPTION: Guy's 13 Kappa
;
US-08-434-000A-12

Query Match          94.4%; Score 518; DB 3; Length 105;
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; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
;
US-09-423-439-51

Query Match          94.9%; Score 521; DB 4; Length 666;
Best Local Similarity 95.2%; Pred. No. 7.4e-39;
Matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPARF 61
Db 156 IVLTQSPAIMASPGKVTITCSASSSVTYMHWFQOKPGTSPKLIYSTSNLASGVPARF 215

QY 62 SGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
Db 216 SGSGSGTSYSLTISRMEADAATYYCQORSTYPLTFGAGTKLEIK 260

RESULT 13
US-08-434-000A-12
; Sequence 12, Application US/08434000A
; Patent No. 6046037
;
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; PRIOR APPLICATION DATA: 08/367,395
; APPLICATION NUMBER: 12/30/94
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; TELEX: SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; TOPOLOGY: DESCRIPTION: Guy's 13 Kappa
;
US-08-434-000A-12

Query Match          94.4%; Score 518; DB 3; Length 105;
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Best Local Similarity 93.3%; Pred. No. 1.9e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
|| :|||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db 1 DIVMTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60

QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 105
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Db 61 FSGSGGTSYSLTISRMEADAATYYCHQRTSYPTYTFGGGTKLEI 105

RESULT 14
US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-351

SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Guy's 13 Kappa
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-312-157-12

Query Match 94.4%; Score 518; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 1.9e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 DIVMTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60

QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 105
|||||||||||||||||||||||||||:||||| |||||
Db 61 FSGSGGTSYSLTISRMEADAATYYCHQRTSYPTYTFGGGTKLEI 105

RESULT 15
US-07-634-278-1
; Sequence 1, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..106
; OTHER INFORMATION: /note= "Variable region of the mouse
; OTHER INFORMATION: anti-Tac antibody light chain."
US-07-634-278-1

Query Match 94.0%; Score 516; DB 1; Length 106;
Best Local Similarity 93.3%; Pred. No. 2.9e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPARF 61
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Db 2 IVLTQSPAIMASPGKVTITCSASSSI SYMHWFQKPGTSPKLIWYTTSNLASGVPARF 61

QY 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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Db 62 SGSGSGTSYSLTISRMEADAATYYCHQRTSYPTLTFGSGTKLEIK 106

Search completed: December 23, 2002, 07:33:20
Job time : 20.1047 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 9.86047 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-23
Perfect score: 549
Sequence: 1 DIELTQSPAIMASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_pep:*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB_pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB_pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB_pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	106	10	US-09-976-787-24 Sequence 24, Appl
2	549	100.0	106	10	US-09-865-198-23 Sequence 23, Appl
3	549	100.0	108	10	US-09-976-787-8 Sequence 8, Appli
4	549	100.0	108	10	US-09-865-198-8 Sequence 8, Appli
5	549	100.0	238	10	US-09-976-787-29 Sequence 29, Appl
6	549	100.0	238	10	US-09-865-198-28 Sequence 28, Appl
7	549	100.0	240	10	US-09-976-787-28 Sequence 28, Appl
8	549	100.0	240	10	US-09-865-198-27 Sequence 27, Appl
9	534	97.3	235	10	US-09-910-059-17 Sequence 17, Appl
10	532	96.9	108	10	US-09-910-059-9 Sequence 9, Appli
11	518	94.4	105	9	US-09-982-107-12 Sequence 12, Appl
12	518	94.4	669	9	US-09-807-721-2 Sequence 2, Appli
13	509	92.7	107	9	US-09-144-886-88 Sequence 88, Appl
14	506	92.2	119	10	US-09-808-037-28 Sequence 28, Appl
15	506	92.2	239	10	US-09-808-037-6 Sequence 6, Appli
16	500	91.1	107	9	US-09-144-886-76 Sequence 76, Appl
17	495	90.2	107	9	US-09-144-886-90 Sequence 90, Appl
18	484	88.2	107	9	US-09-144-886-75 Sequence 75, Appl
19	484	88.2	107	9	US-09-144-886-78 Sequence 78, Appl

20	479	87.2	107	9	US-09-144-886-82	Sequence 82, Appl
21	479	87.2	107	9	US-09-144-886-83	Sequence 83, Appl
22	479	87.2	109	9	US-09-144-886-91	Sequence 91, Appl
23	478	87.1	131	10	US-09-881-823-6	Sequence 6, Appli
24	475.5	86.6	112	9	US-09-144-886-89	Sequence 89, Appl
25	466	84.9	109	9	US-09-144-886-96	Sequence 96, Appl
26	463	84.3	106	10	US-09-158-120A-35	Sequence 35, Appl
27	461	84.0	106	10	US-09-965-099-105	Sequence 105, App
28	461	84.0	106	12	US-10-051-852-105	Sequence 105, App
29	461	84.0	107	10	US-09-965-099-11	Sequence 11, Appl
30	461	84.0	107	12	US-10-051-852-11	Sequence 11, Appl
31	461	84.0	109	9	US-09-144-886-79	Sequence 79, Appl
32	461	84.0	112	10	US-09-965-099-103	Sequence 103, App
33	461	84.0	112	12	US-10-051-852-103	Sequence 103, App
34	460	83.8	109	9	US-09-144-886-97	Sequence 97, Appl
35	454	82.7	109	9	US-09-144-886-77	Sequence 77, Appl
36	454	82.7	109	9	US-09-144-886-98	Sequence 98, Appl
37	453	82.5	107	10	US-09-910-059-71	Sequence 71, Appl
38	453	82.5	235	10	US-09-910-059-99	Sequence 99, Appl
39	449	81.8	127	10	US-09-753-436-80	Sequence 80, Appl
40	448	81.6	106	10	US-09-893-615-89	Sequence 89, Appl
41	442	80.5	107	10	US-09-910-059-61	Sequence 61, Appl
42	440	80.1	107	10	US-09-910-059-50	Sequence 50, Appl
43	440	80.1	235	10	US-09-910-059-52	Sequence 52, Appl
44	437	79.6	109	9	US-09-144-886-92	Sequence 92, Appl
45	432	78.7	107	10	US-09-910-059-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match	100.0%;	Score 549;	DB 10;	Length 106;
Best Local Similarity	100.0%;	Pred. No. 5.3e-31;		
Matches 106;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYTSNLASGVPAR	60	
Db	1	DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYTSNLASGVPAR	60	
QY	61	FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK	106	
Db	61	FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK	106	

RESULT 2
US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping

```
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match      100.0%; Score 549; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.3e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
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QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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RESULT 3
US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match      100.0%; Score 549; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.4e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
   |||||
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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RESULT 4
US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
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; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match      100.0%; Score 549; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.4e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
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QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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RESULT 5
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match      100.0%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 9.8e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
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Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 192
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QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
   |||||
Db 193 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238
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RESULT 6
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
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; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 9.8e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
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Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 192
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QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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Db 193 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238
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RESULT 7
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 549; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 9.9e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
|||||
Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 192
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QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 193 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238
|||||

RESULT 8
US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 549; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 9.9e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
|||||
Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 192
|||||

QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 193 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238
|||||

RESULT 9
US-09-910-059-17
; Sequence 17, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric light chain sequence
US-09-910-059-17

Query Match 97.3%; Score 534; DB 10; Length 235;
Best Local Similarity 96.2%; Pred. No. 9.8e-30;
Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
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Db 23 DIELTQSPAIMSASPGKVTITCSASSSVTYMHWFQKPGTSPKLIYSTSNLASGVPAR 82
|||||

QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 83 FSGSGGTSYSLTISRMEADAATYYCQQRSTYPLTFGAGTKLEIK 128
|||||

RESULT 10
US-09-910-059-9
; Sequence 9, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System

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; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-9
Query Match          96.9%; Score 532; DB 10; Length 108;
Best Local Similarity 95.3%; Pred. No. 7.4e-30;
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
|||||
Db 1 DIELTQSPAIMASPGKVTITCSASSSVTYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
|||||

QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEIK 106
|||||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSTYPLTFGAGTKLELK 106
|||||

RESULT 11
US-09-982-107-12
; Sequence 12, Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12
Query Match          94.4%; Score 518; DB 9; Length 105;
Best Local Similarity 93.3%; Pred. No. 6.3e-29;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
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Db 1 DIVMTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
|||||

QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEI 105
|||||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCHQRTSYPTYTFFGSGTKLEI 105
|||||

RESULT 12
US-09-807-721-2
; Sequence 2, Application US/09807721
; Patent No. US20020174453A1
; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY
```

```
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,721
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-721-2
Query Match          94.4%; Score 518; DB 9; Length 669;
Best Local Similarity 92.5%; Pred. No. 2.5e-28;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
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Db 457 DIVMTQSPAIMASPGKVTITCSASSMVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 516
|||||

QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSGTKLEIK 106
|||||
Db 517 FSGSGSGTSYSLTISRMEAEADAATYYCHQRTSYPTYTFFGSGTKLEIK 562
|||||

RESULT 13
US-09-144-886-88
; Sequence 88, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/a clone
US-09-144-886-88
Query Match          92.7%; Score 509; DB 9; Length 107;
Best Local Similarity 97.0%; Pred. No. 2.5e-28;
Matches 97; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
|||||
Db 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGVPAR 60
|||||

QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGSG 100
|||||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYPFTFGGG 100
|||||

RESULT 14
US-09-808-037-28
; Sequence 28, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
```


FILE REFERENCE: SOLOMON=2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH: 119
TYPE: PRT
ORGANISM: synthetic construct
US-09-808-037-28

Query Match 92.2%; Score 506; DB 10; Length 119;
Best Local Similarity 90.6%; Pred. No. 4.4e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 14 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 73
QY 61 FSGSGSGTSYSLTISRMEADAATYQCQRSSYPFTFGSGTKLEIK 106
Db 74 FSGSGSGTSYSLTISRMEADAATYCHQRSSYPFTFGGGAKLEIK 119

RESULT 15
US-09-808-037-6
Sequence 6, Application US/09808037
Patent No. US20020052311A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON=2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-808-037-6

Query Match 92.2%; Score 506; DB 10; Length 239;
Best Local Similarity 90.6%; Pred. No. 7.4e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 134 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 193
QY 61 FSGSGSGTSYSLTISRMEADAATYQCQRSSYPFTFGSGTKLEIK 106
Db 194 FSGSGSGTSYSLTISRMEADAATYCHQRSSYPFTFGGGAKLEIK 239

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 20.9535 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-23
Perfect score: 549
Sequence: 1 DIELTQSPAIMASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	513	93.4	106	2 B54378	Ig light chain V r
2	508	92.5	140	2 PL0013	Ig kappa chain pre
3	483	88.0	130	2 A32513	Ig kappa chain pre
4	483	88.0	132	2 S05268	Ig kappa chain pre
5	482	87.8	107	2 PC4405	Ig kappa chain V r
6	481	87.6	99	2 D38601	Ig kappa chain V r
7	476	86.7	107	2 A30562	Ig kappa chain V r
8	474	86.3	106	2 G27887	Ig kappa chain V r
9	472	86.0	106	2 PS0070	Ig kappa chain V r
10	471	85.8	107	2 B30562	Ig kappa chain V r
11	470	85.6	105	2 S26338	Ig kappa chain V r
12	465	84.7	103	2 S29591	Ig kappa chain V r
13	465	84.7	108	2 PL0278	Ig kappa chain V r
14	464	84.5	130	1 JL0079	Ig kappa chain pre
15	463	84.3	106	2 PS0071	Ig kappa chain V r
16	461	84.0	104	2 B49049	Ig kappa chain V r
17	461	84.0	108	2 PL0276	Ig kappa chain V r
18	461	84.0	108	2 PL0277	Ig kappa chain V r
19	461	84.0	120	2 S66536	Ig light chain V r
20	460	83.8	107	2 PD0011	Ig kappa chain V r
21	459.5	83.7	108	2 G30560	Ig kappa chain V r
22	458	83.4	91	2 S17626	Ig kappa chain pre
23	455	82.9	130	2 B32456	Ig kappa chain V r
24	453	82.5	108	2 PS0069	Ig kappa chain pre
25	451	82.1	235	2 S25058	Ig kappa chain - m
26	450	82.0	91	2 S17630	Ig kappa chain V r
27	450	82.0	104	2 JC6076	anti-D-dimer monoc
28	450	82.0	107	2 A42848	Ig light chain V r
29	450	82.0	107	2 PT0406	Ig kappa chain V r

30	448	81.6	107	2 S11119	Ig kappa chain V r
31	448	81.6	120	2 A34871	Ig kappa chain V r
32	447	81.4	107	2 S11118	Ig kappa chain V r
33	446.5	81.3	108	2 S38720	Ig light chain V r
34	446	81.2	100	2 S29590	Ig kappa chain V r
35	446	81.2	108	2 S29581	Ig kappa chain V r
36	446	81.2	130	2 S04573	Ig kappa chain pre
37	444	80.9	123	2 S05269	Ig kappa chain pre
38	443	80.7	107	2 PT0401	Ig light chain V r
39	441	80.3	106	2 PL0082	Ig kappa chain V r
40	441	80.3	107	2 PT0398	Ig light chain V r
41	440	80.1	97	2 S26341	Ig light chain V r
42	440	80.1	107	2 S11121	Ig kappa chain V r
43	437	79.6	107	2 PT0402	Ig light chain V r
44	436	79.4	97	2 PH1085	Ig light chain V r
45	436	79.4	99	2 S29585	Ig kappa chain V r

ALIGNMENTS

RESULT 1

B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: B54378

R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluor

A;Reference number: A54378; MUID:94165109; PMID:7509814

A;Accession: B54378

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <AGA>

A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747

A;Experimental source: spleen and myeloma cell line MOPC 315.43

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 513; DB 2; Length 106;
Best Local Similarity 94.3%; Pred. No. 6.5e-35;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPCTSPKLWIYSTSNLASGVPARF 61

Db 2 IVLTQSPAIMASPGKVTITCSASSSVSYMHWFQKPCTSPKLWIYSTSKLASGVPARF 61

QY 62 SCGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

Db 62 SCGSGGTSYSLPISRMEADAATYYCQQRSSYPITFGAGTKLELK 106

RESULT 2

PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C;Accession: PL0013

R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424

A;Accession: PL0013

A;Molecule type: mRNA

A;Residues: 1-140 <CHE>

A;Experimental source: cell line 4C11

C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Db 62 SGGSGTSYSLTSSMEAEATAATYCCQWSSNPVTFGAPTKELEK 106

Job time : 21.9535 secs

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FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 77.2%; Score 424; DB 1; Length 107;
Best Local Similarity 81.3%; Pred. No. 9.3e-36;
Matches 87; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPWIYEISKLASGVPAR 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYP-FTFGSGTKLEIK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQ-WNYPLITFGGGTKLEIK 106
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RESULT 10
KV6C_MOUSE
ID KV6C_MOUSE STANDARD; PRT; 107 AA.
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region TEP C 601/TEPC 191.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 601).
RX MEDLINE=79082830; Pubmed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RL proteins.";
RN [2]
RP SEQUENCE (TEPC 191).
RX MEDLINE=81054757; Pubmed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "kappa Chain joining segments and structural diversity of antibody
RL combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -!- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
CC THAT BIND GALACTAN.
DR PIR; A01941; KVMXS4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match 77.0%; Score 423; DB 1; Length 107;
Best Local Similarity 80.4%; Pred. No. 1.2e-35;
Matches 86; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPWIYEISKLASGVPAR 60
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QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQORSSYP-FTFGSGTKLEIK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQ-WNYPLITFGAGTKLELK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
KV6E_MOUSE
ID KV6E_MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; Pubmed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RL combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; Pubmed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an x-ray diffraction
RL study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01942; KVMJS5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87
FT STRAND 4 7
FT STRAND 10 14
FT TURN 15 16
FT STRAND 19 25
FT STRAND 31 37
FT TURN 39 40
FT STRAND 44 48
FT TURN 49 51
FT STRAND 52 53
FT TURN 55 56
FT TURN 59 60
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 74
FT HELIX 79 81
FT STRAND 83 91
FT TURN 92 93
FT STRAND 94 97
FT STRAND 101 106
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;
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RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 67.1%; Score 368.5; DB 1; Length 111;
Best Local Similarity 64.9%; Pred. No. 3.4e-30;
Matches 72; Conservative 14; Mismatches 20; Indels 5; Gaps 1;

QY 1 DIELTQSPALMSASPGKVTITCSASSV-----SYMHWFQOKPGTSPKLIWYSTSNLAS 55
|| ||||| :| |:: ||:| || || ||||:| |||| || ||: ||| |
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYMNWYQKPGPKLLIYTASNLES 60

QY 56 GVPARFSGSGSTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSNEDPWTFGSGTKLEIK 111

RESULT 15
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 66.8%; Score 366.5; DB 1; Length 111;
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Best Local Similarity 64.0%; Pred. No. 5.3e-30;
Matches 71; Conservative 14; Mismatches 21; Indels 5; Gaps 1;

QY 1 DIELTQSPALMSASPGKVTITCSASSV-----SYMHWFQOKPGTSPKLIWYSTSNLAS 55
|| ||||| :| |:: ||:| || || ||||:| |||| || ||: ||| |
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGTGESYMNWYQQNPGQSPKLLIYAASNLES 60

QY 56 GVPARFSGSGSTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|:||||| ||||| :| | :| ||||| ||||| :| |||| |||||
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSNEDPYTFGGGTKLEIK 111

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 43.9612 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-23
Perfect score: 549
Sequence: 1 DIELTQSPAIMASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493	89.8	134	11 Q8VDD0	Q8vdd0 mus musculu
2	470	85.6	106	5 Q9U410	Q9u410 schistosoma
3	434.5	79.1	97	11 Q9JL76	Q9jl76 mus musculu
4	433	78.9	235	11 Q91W12	Q91wl2 mus musculu
5	403.5	73.5	101	11 Q9JL78	Q9jl78 mus musculu
6	371.5	67.7	234	11 Q8R062	Q8r062 mus musculu
7	365.5	66.6	111	11 Q920E9	Q920e9 mus musculu
8	362.5	66.0	214	11 Q9RIA5	Q9rla5 mus musculu
9	360.5	65.7	108	4 Q9UL77	Q9ul77 homo sapien
10	356	64.8	107	4 Q96SA9	Q96sa9 homo sapien
11	356	64.8	109	4 Q9UL78	Q9ul78 homo sapien
12	354.5	64.6	108	4 Q9UL70	Q9ul70 homo sapien
13	352.5	64.2	108	4 Q9UL79	Q9ul79 homo sapien
14	348	63.4	107	4 Q9UL81	Q9ul81 homo sapien
15	347.5	63.3	234	11 Q91WF8	Q91wf8 mus musculu
16	347.5	63.3	234	11 Q8VCP0	Q8vcp0 mus musculu

17	345.5	62.9	233	11 Q91WS9	Q91ws9 mus musculu
18	342.5	62.4	107	11 Q9JL84	Q9jl84 mus musculu
19	342.5	62.4	298	11 Q9QYF0	Q9qyf0 mus musculu
20	341.5	62.2	108	4 Q9UL83	Q9ul83 homo sapien
21	338.5	61.7	109	11 Q920E6	Q920e6 mus musculu
22	337	61.4	109	4 Q9UL86	Q9ul86 homo sapien
23	332.5	60.6	108	11 Q8VIJ0	Q8vij0 mus musculu
24	332	60.5	109	4 Q9UL85	Q9ul85 homo sapien
25	322	58.7	238	11 Q99M37	Q99m37 mus musculu
26	321.5	58.6	127	11 Q925S9	Q925s9 mus musculu
27	315.5	57.5	116	4 Q96PF6	Q96pf6 homo sapien
28	314	57.2	238	11 Q8VCI6	Q8vci6 mus musculu
29	308.5	56.2	103	11 Q9JL80	Q9jl80 mus musculu
30	304	55.4	239	11 Q8VC55	Q8vc55 mus musculu
31	302	55.0	239	4 Q8TCD0	Q8tcd0 homo sapien
32	300.5	54.7	107	11 Q9ERZ9	Q9erz9 mus musculu
33	297	54.1	104	11 Q9JL82	Q9jl82 mus musculu
34	292.5	53.3	99	11 Q9JL74	Q9jl74 mus musculu
35	290.5	52.9	114	4 Q9UL80	Q9ul80 homo sapien
36	286	52.1	241	11 Q921A6	Q921a6 mus musculu
37	281	51.2	237	4 Q8WTU6	Q8wtu6 homo sapien
38	277.5	50.5	234	11 Q8R028	Q8r028 mus musculu
39	276	50.3	237	4 Q8WUK4	Q8wuk4 homo sapien
40	260.5	47.4	109	6 Q9N0W5	Q9n0w5 oryctolagus
41	259	47.2	233	4 Q8TBC9	Q8tbc9 homo sapien
42	247.5	45.1	236	4 Q96E61	Q96e61 homo sapien
43	244	44.4	107	4 Q9NSD6	Q9nsd6 homo sapien
44	244	44.4	110	4 Q8TE63	Q8te63 homo sapien
45	243	44.3	108	4 Q96SB0	Q96sb0 homo sapien

ALIGNMENTS

RESULT 1
Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Sembi P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;

Query Match 89.8%; Score 493; DB 11; Length 134;
Best Local Similarity 89.5%; Pred. No. 2.4e-44;
Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSLASGVPARF 61

Db 24 IVLTQSPAIMSASPGEKVTMTCSASSSISYMHVYQQKPGTSPKRWIYDTSKLASGVPARF 83
QY 62 SGSGSGTSYSLTISRMEAEADAATYCCQORSSYPFTFGSGTKLEIK 106
Db 84 SGSGSGTSYSLTISRMEAEADAATYCHQRSSYPWTFGGGTKLEIK 128
RESULT 2
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Peng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;
Query Match 85.6%; Score 470; DB 5; Length 106;
Best Local Similarity 87.4%; Pred. No. 4.8e-42;
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 4 LTQSPAIMSASPGEKVTITCSASSSVSYMHVYQQKPGTSPKRWIYSTSNLASGVPARFSG 63
Db 4 LTQSPAIMSASPGEKVTMTCSASSSVYVYWLQKPGSPRLIYDTSNLASGVVPRFSG 63
QY 64 SGSGTSYSLTISRMEAEADAATYCCQORSSYPFTFGSGTKLEIK 106
Db 64 SGSGTSYSLTISRMEAEADAATYCCQWTSYPFTFGSGTKLEIK 106
RESULT 3
Q9JL76
ID Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).

DR EMBL; AF206030; AAF69328.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;
Query Match 79.1%; Score 434.5; DB 11; Length 97;
Best Local Similarity 86.6%; Pred. No. 2.3e-38;
Matches 84; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
QY 11 MSASPGEKVTITCSASSSVSYMHVYQQKPGTSPKRWIYSTSNLASGVPARFSGSGTSY 70
Db 1 LSASPGEKVTMTCRASSSVSYMHVYQQKPGSSPKRWIYATSNLASGVPARFSGSGTSY 60
QY 71 SLTISRMEAEADAATYCCQORSS-YPFTFGSGTKLEIK 106
Db 61 SLTISRVEAEADAATYCCQWSSKYMFTFGGGTKLEIK 97
RESULT 4
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
Query Match 78.9%; Score 433; DB 11; Length 235;
Best Local Similarity 81.0%; Pred. No. 9.7e-38;
Matches 85; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
QY 2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHVYQQKPGTSPKRWIYSTSNLASGVPARF 61
Db 24 IVLTQSPAIMSASPGERVTMTCSASSSVSHMHVYQQKSGTSPKRWIYDTFKLTSGVDPDRF 83
QY 62 SGSGSGTSYSLTISRMEAEADAATYCCQORSSYPFTFGSGTKLEIK 106
Db 84 SGSGSGTSYSLTISRMEAEADVATYCCQWSRNPPTFGVGTGKLEIK 128
RESULT 5
Q9JL78
ID Q9JL78 PRELIMINARY; PRT; 101 AA.
AC Q9JL78;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

	Matches	67	Conservative	19	Mismatches	20	Indels	1	Gaps	1
QY	1	DIELTQSPAIMSASPGKVTITCSASSVS-YMHWFOQKPGTSPKLWIYSTSNLASGYPA 59								
Db	21	DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS 80								
QY	60	RFGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106								
Db	81	RFGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVK 127								

Search completed: December 23, 2002, 07:29:59
Job time : 43.612 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 4.8314 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	21 AAY97234	Complementary dete
2	48	100.0	9	22 AAE13142	Humanised antibody
3	48	100.0	9	22 AAB82708	VEGF antagonist an
4	48	100.0	9	22 AAG63993	Complementarity de
5	48	100.0	9	23 AAU74411	Light chain comple
6	48	100.0	106	22 AAE13144	Humanised antibody
7	48	100.0	106	23 AAU74418	Antigen-binding pr
8	48	100.0	107	22 AAG63987	Amino acid sequenc
9	48	100.0	108	21 AAY97236	Variable light cha
10	48	100.0	108	22 AAB82710	VEGF antagonist an

11	48	100.0	108	23 AAU74413	Antigen-binding pr
12	48	100.0	125	22 AAE13146	Chimeric pLC11 lig
13	48	100.0	125	22 AAB82702	VEGF antagonist an
14	48	100.0	238	23 AAU74420	Antigen-binding pr
15	48	100.0	240	23 AAU74419	Antigen-binding pr
16	48	100.0	330	22 AAB70842	SNV-env leader/hum
17	45	93.8	9	19 AAW73171	CDR3 of light chai
18	45	93.8	9	20 AAY28392	Peptide fragment f
19	45	93.8	9	22 AAB83165	Mouse ganglioside
20	45	93.8	107	22 AAB83159	Mouse ganglioside
21	45	93.8	107	22 AAB83167	Ganglioside GM2 an
22	45	93.8	129	15 AAR53329	KM-796 and KM-750
23	45	93.8	129	20 AAY28385	Anti-GM2 light cha
24	45	93.8	129	20 AAY28357	Antibody chain use
25	45	93.8	130	19 AAW73179	Fragment of gangli
26	45	93.8	130	19 AAW73180	Fragment of gangli
27	45	93.8	130	19 AAW73181	Fragment of gangli
28	45	93.8	130	19 AAW73182	Fragment of gangli
29	45	93.8	130	19 AAW73183	Fragment of gangli
30	45	93.8	130	19 AAW73184	Fragment of gangli
31	45	93.8	130	19 AAW73185	Fragment of gangli
32	45	93.8	130	19 AAW73173	Light chain of gan
33	45	93.8	130	19 AAW73174	Light chain of gan
34	45	93.8	130	19 AAW73176	Light chain of gan
35	45	93.8	130	20 AAY28375	Human chimeric ant
36	45	93.8	130	20 AAY28376	Human chimeric ant
37	45	93.8	130	20 AAY28377	Human chimeric ant
38	45	93.8	130	20 AAY28378	Human chimeric ant
39	45	93.8	130	20 AAY28379	Human chimeric ant
40	45	93.8	130	20 AAY28380	Human chimeric ant
41	45	93.8	130	20 AAY28381	Human chimeric ant
42	45	93.8	130	20 AAY28382	Human chimeric ant
43	45	93.8	130	20 AAY28383	Human chimeric ant
44	45	93.8	133	15 AAR53345	REI human Ab L cha
45	45	93.8	133	20 AAY28394	Anti-GM2 light cha

ALIGNMENTS

RESULT 1
AAY97234
ID AAY97234 standard; Protein; 9 AA.
XX AAY97234;
AC AAY97234;
XX 19-DEC-2000 (first entry)
DT Complementary determining region (CDRL3) of anti-SI(KDR) antibody.
XX Immunoglobulin; antibody; complementary determining region; CDR;
DE VEGF; vascular endothelial growth factor; KDR;
XX kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Karposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX Homo sapiens.
OS Synthetic.
OS WO200044777-A1.
XX 03-AUG-2000.
PD 28-JAN-2000; 2000WO-US02180.
XX 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX (IMCL-) IMCLONE SYSTEMS INC.
PA Zhu Z, Witte L;
PI

XX WPI; 2000-505966/45.
DR N-PSDB; AAN53766.
XX
PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 3; Page 50; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
Db 1 QQRSSYPFT 9
RESULT 2
AAE13142
ID AAE13142; standard; peptide; 9 AA.
XX
AC AAE13142;
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody murine light chain hypervariable region (VL) CDR3.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain hypervariable region; VL; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.
XX
OS Mus sp.
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafil S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21668.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -

XX Claim 8; Page 15; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody murine light chain hypervariable region (VL) CDR-3 used in the
CC exemplification of the invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
Db 1 QQRSSYPFT 9
RESULT 3
AAB82708
ID AAB82708 standard; Peptide; 9 AA.
XX
AC AAB82708;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 VL CDR-3.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
KW complementarity determining region.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
PS Disclosure; Page 37; 42pp; English.
XX

CC The present sequence is that of complementarity determining region
CC 3 of the light chain variable region (see also AAB82702) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db ||||||
1 QQRSSYPFT 9

RESULT 4
AAG63993
ID AAG63993 standard; peptide; 9 AA.
XX
AC AAG63993;
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region of light chain of antibody 2C4.
XX
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX
PN WO200166126-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07193.
XX
PR 07-MAR-2000; 2000US-0187595.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX
DR WPI; 2001-570749/64.
XX
PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal
XX
PS Claim 10; Page 34; 35pp; English.
XX
CC AAG63991-93 represent the complementarity determining regions (CDRs)
CC of the light chain variable region of murine monoclonal antibody 2C4.

CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The
CC antibody is useful for treating or preventing allergic rhinitis,
CC allergies, asthma, anemia, eczema or diseases such as lymphoma,
CC leukemia or systemic mastocytosis in a mammal. It is also useful for
CC detecting the presence of a cell, especially eosinophil in a sample,
CC by detecting binding of the antibody to SAF-2. The antibody can be
CC coupled to toxins, antiproliferative drugs or radionuclides to
CC kill cells in areas of excessive SAF-2 expression.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db ||||||
1 QQRSSYPFT 9

RESULT 5
AAU74411
ID AAU74411 standard; peptide; 9 AA.
XX
AC AAU74411;
XX
DT 26-MAR-2002 (first entry)
XX
DE Light chain complementarity determining region L3 (CDRL3).
XX
KW Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody light chain variable domain.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20282.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 55; Page 57; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the light chain variable domain
CC complementarity determining region L3 (CDRL3) incorporated into an
CC antigen-binding protein described in the method of the invention.

SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 1 QQRSSYPFT 9

RESULT 6
AAE13144
ID AAE13144 Standard; Protein; 106 AA.

AC AAE13144
XX 28-JAN-2002 (first entry)

DE Humanised antibody light chain fragment.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytotstatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.

XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.

XX WO200174296-A2.
PN 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

DR WPI; 2001-662942/76.
DR N-PSDB; AAD21670.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -

PS Claim 8; Page 16; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody light chain fragment used in the exemplification of the
CC invention.

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 48; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 88 QQRSSYPFT 96

RESULT 7
AAU74418
ID AAU74418 standard; peptide; 106 AA.

XX AC AAU74418;

XX 26-MAR-2002 (first entry)

DE Antigen-binding protein light chain variable domain (VH) #2.

XX Antigen-binding protein; antibody light chain variable domain;
KW cytotstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.

XX Mus sp.

XX WO200190192-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US16924.

XX 24-MAY-2000; 2000US-206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z;

XX WPI; 2002-106189/14.
DR N-PSDB; AAU20289.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides

PS Claim 61; Page 61; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a light chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.

XX AAB82710;
AC 15-OCT-2001 (first entry)
DT VEGF antagonist antibody IMC-1C11 light chain variable region.
XX
DE IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
XX
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.
XX
OS Chimeric Mus sp.
OS Chimeric Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24..33
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT Region 49..55
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT Region 88..96
FT /label= CDR-L3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26406.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent
XX
PS Disclosure; Page 38-39; 42pp; English.
XX
CC The present sequence is that of the light chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 48; DB 22; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
Db 88 QQRSSYPFT 96
RESULT 11
AAU74413
ID AAU74413 standard; peptide; 108 AA.
XX
AC AAU74413;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein light chain variable domain (VH) #1.
XX
KW Antigen-binding protein; antibody light chain variable domain;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20284.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 57; Page 57; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a light chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 48; DB 23; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | | | |
Db 88 QQRSSYPFT 96

RESULT 12
AAE13146
ID AAE13146 standard; Protein; 125 AA.
XX
AC AAE13146;
XX
DT 28-JAN-2002 (first entry)
XX
DE Chimeric p1C11 light chain fragment.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human; p1C11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader_peptide
FT Protein 20..125
FT /note= "Mature chimeric p1C11 light chain fragment"
FT Region 43..52
FT /label= CDR_L1
FT Region 68..74
FT /label= CDR_L2
FT Region 107..115
FT /label= CDR_L3
XX WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Raf11 S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21683.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to

CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1C11 light chain fragment which is used for the construction of chimeric
CC p1C11 IgG expression vector. Chimeric p1C11 light chain contains cloned
CC variable light chain (VL) and human kappa light chain constant region
CC (CL).
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 48; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | | | |
Db 107 QQRSSYPFT 115

RESULT 13
AAB82702
ID AAB82702 standard; Protein; 125 AA.
XX
AC AAB82702;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 light chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..125
FT /label= Mature_protein
FT Region 43..52
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT Region 68..74
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT Region 107..115
FT /label= CDR-L3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26414.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -

XX Disclosure; Fig 1; 42pp; English.

PS The present sequence is that of the light chain variable region of

XX IMC-1C11, a mouse-human chimeric antibody that has vascular

CC endothelial growth factor (VEGF) antagonist activity. The antibody,

CC or a fragment of it, can be used as an anti-angiogenic molecule,

CC together with a chemotherapeutic acid, for the treatment of an

CC angiogenic dependent condition in a mammal, especially a human.

CC The invention relates generally to a method of treating or

CC controlling an angiogenic dependent condition by administering an

CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a

CC regression or arrest of the condition while minimising or

CC preventing significant toxicity of the chemotherapeutic agent.

CC The anti-angiogenic molecule inhibits or blocks the action of a

CC vascular endothelium survival factor such as VEGF or its receptor,

CC and is especially IMC-1C11. Conditions that can be treated include

CC a neoplasm, a collagen-vascular disease or an autoimmune disease,

CC especially a solid tumour, including breast carcinoma, lung

CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,

CC ovarian carcinoma, neuroblastoma, central nervous system tumour,

CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX

SQ Sequence 125 AA;

Query Match 100.0%; Score 48; DB 22; Length 125;

Best Local Similarity 100.0%; Pred. No. 0.086;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 107 QQRSSYPFT 115

RESULT 14

AAU74420

ID AAU74420: standard; Protein; 238 AA.

XX

AC AAU74420;

XX

DT 26-MAR-2002 (first entry)

XX

DE Antigen-binding protein, single chain variable fragment version #2.

XX

KW Antigen-binding protein; single chain variable fragment; svFv; antigen;

KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.

XX

OS Mus sp.

OS Synthetic.

XX

FH Key

FT Region

FT

FT Location/Qualifiers

FT 1..117

FT /label= VH

FT /note= "Heavy chain variable domain. Specifically

FT claimed in claim 61"

FT 118..132

FT /label= Linker

FT /note= "15 amino acid linker joins the VH and VL

FT regions of the single chain variable fragment

FT protein. Encoded by AAS20285"

FT Region

FT 133..238

FT /label= VL

FT /note= "Light chain variable domain. Specifically

FT claimed in claim 61"

XX

PN WO200190192-A2.

XX

PD 29-NOV-2001.

XX

PF 24-MAY-2001; 2001WO-US16924.

XX

PR 24-MAY-2000; 2000US-206749P.

XX

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

XX

DR WPI; 2002-106189/14.

XX

PT New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX

PS Claim 63; Page 62-63; 64pp; English.

XX

CC The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

CC light chain constant domain (CL domain), and P2 has an antigen-binding

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC neutralising the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogenous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This is the amino acid sequence of a single chain variable fragment

CC (scFv), an engineered protein containing a variable light and variable

CC heavy domain on one polypeptide, described in the method of the

CC invention.

XX

SQ Sequence 238 AA;

Query Match 100.0%; Score 48; DB 23; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 220 QQRSSYPFT 228

RESULT 15

AAU74419

ID AAU74419 standard; Protein; 240 AA.

XX

AC AAU74419;

XX

DT 26-MAR-2002 (first entry)

XX

DE Antigen-binding protein, single chain variable fragment version #1.

XX

KW Antigen-binding protein; single chain variable fragment; scFv; antigen;

KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.

XX

OS Mus sp.

OS Synthetic.

XX

FH Key

FT Region

FT

FT Location/Qualifiers

FT 1..117

FT /label= VH

FT /note= "Heavy chain variable domain. Specifically

FT claimed in claim 57"

FT 118..132

FT Region

FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 63; Page 62; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
CC invention.
XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 48; DB 23; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | | |
Db 220 QQRSSYPFT 228

Search completed: December 23, 2002, 07:25:06
Job time : 4.8314 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 62.8081 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQQSGAELVSGASVKL.....AAYGDYEGYWGQGTTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	117	AAE13143	Humanised antibody
2	631	100.0	117	AAB82709	VEGF antagonist an
3	631	100.0	117	AAU74417	Antigen-binding pr
4	631	100.0	136	AAB82701	VEGF antagonist an
5	631	100.0	238	AAU74420	Antigen-binding pr
6	624	98.9	117	AAU97235	Variable heavy cha
7	624	98.9	117	AAU74412	Antigen-binding pr
8	624	98.9	240	AAU74419	Antigen-binding pr
9	619	98.1	136	AAE13145	Chimeric p1C11 hea
10	558.5	88.5	535	AAW28491	Human p53 protein

11	558.5	88.5	535	18	AAW28492	Human p53 protein
12	554.5	87.9	116	21	AAV70787	Murine anti-p53 mo
13	553.5	87.7	243	19	AAW60769	Single chain antib
14	536.5	85.0	112	20	AAW89173	Anti-p53 monoclonal
15	536.5	85.0	118	18	AAW01586	Lead binding MAB 1
16	517.5	82.0	270	16	AAW75719	MFE-23 antibody.
17	517.5	82.0	556	22	AAU97935	scFv-rearranged ca
18	517.5	82.0	556	22	AAU80040	scFv-rearranged ca
19	511.5	81.1	124	15	AAAR60566	Anti-carcinoembryo
20	511.5	81.1	249	19	AAW60770	Single chain antib
21	511.5	81.1	553	18	AAW11508	Single chain anti-
22	511.5	81.1	553	20	AAW73223	H22-anti-CEA antib
23	511.5	81.1	553	22	AAW85455	Bispecific single
24	511.5	81.1	553	22	AAW61960	Bispecific single
25	506.5	80.3	124	15	AAAR60565	Anti-carcinoembryo
26	505.5	80.1	116	13	AAAR24807	RSV19 VH. Mus mus
27	504.5	80.0	116	14	AAAR42804	RSV19 heavy chain
28	503.5	79.8	124	20	AAV39528	Murine COL1 VH cha
29	503.5	79.8	124	23	AAU76632	Murine Col-1(CEA a
30	502.5	79.6	120	18	AAW41387	Anti-CEA antibody
31	502.5	79.6	255	18	AAW41394	Chimeric anti-CEA
32	502.5	79.6	281	20	AAW82744	Fusion protein p1C
33	502.5	79.6	642	20	AAW82741	806.077 heavy chai
34	502.5	79.6	666	20	AAW82745	Fusion protein (80
35	501.5	79.5	116	14	AAAR42802	RSV19 heavy chain
36	495	78.4	119	12	AAAR14394	H3 region of MAB T
37	495	78.4	119	19	AAW48758	TAl antibody VH ch
38	494	78.3	119	12	AAAR14395	Modified H3 region
39	488	77.3	140	12	AAAR11384	Variable gamma hea
40	487.5	77.3	258	23	ABB05962	Monoclonal antibod
41	487.5	77.3	258	23	ABB05990	Mouse monoclonal a
42	487.5	77.3	258	23	ABB05994	Mouse and human ch
43	487.5	77.3	287	23	ABB05982	Monoclonal antibod
44	485.5	76.9	120	16	AAAR79889	Anti-EGFR antibody
45	482.5	76.5	136	22	AAW35290	Murine PSCA antibo

ALIGNMENTS

RESULT 1

AAE13143

ID AAE13143 standard; Protein; 117 AA.

XX AAE13143;

DT 28-JAN-2002 (first entry)

XX Humanised antibody heavy chain fragment.

DE Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX WO200174296-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.

PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.

DR N-PSDB; AAD21669.

CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.

XX
SQ Sequence 117 AA;
Query Match 98.9%; Score 624; DB 21; Length 117;
Best Local Similarity 99.1%; Pred. No. 5.3e-47;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIDPENGDSY 60
Db 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIDPENGDSGY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117
Db 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117

RESULT 7
AAU74412
ID AAU74412 standard; peptide; 117 AA.
XX AAU74412;
AC AAU74412;
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein heavy chain variable domain (VH) #1.
XX
KW Antigen-binding protein; antibody heavy chain variable domain;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20283.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 57; Page 57; 64pp; English.
XX

CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.

XX
SQ Sequence 117 AA;
Query Match 98.9%; Score 624; DB 23; Length 117;
Best Local Similarity 99.1%; Pred. No. 5.3e-47;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIDPENGDSY 60
Db 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIDPENGDSGY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117
Db 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117

RESULT 8
AAU74419
ID AAU74419 standard; Protein; 240 AA.
XX AAU74419;
AC AAU74419;
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #1.
XX
KW Antigen-binding protein; single chain variable fragment; scFv; antigen;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"
FT
FT Region 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT
FT Region 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX

PI Zhu Z;
XX WPI; 2002-106189/14.
DR
XX
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 63; Page 62; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
CC invention.
XX
SQ Sequence 240 AA;
Query Match 98.9%; Score 624; DB 23; Length 240;
Best Local Similarity 99.1%; Pred. No. 1.1e-46;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSY 60
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSY 60
Qy 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGYEGYWGQTTVTSS 117
Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGYEGYWGQTTVTSS 117
RESULT 9
AAE13145
ID AAE13145 standard; Protein; 136 AA.
XX
AC AAE13145;
XX
DT 28-JAN-2002 (first entry)
XX
DE Chimeric p1c11 heavy chain fragment.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human p1c11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader_peptide
FT Protein 20..136
FT /note= "Mature chimeric p1c11 heavy chain fragment"
FT Region 45..54

FT /label= CDR_H1
FT 69..85
FT /label= CDR_H2
FT Misc-difference 84
FT /note= "Residue 'O' is present at this location in the
FT sequence shown in fig-11 of the specification"
FT Misc-difference 101
FT /note= "Residue 'O' is present at this location in the
FT sequence shown in fig-11 of the specification"
FT 119..125
FT /label= CDR_H3
FT
XX WO200174296-A2.
XX
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafii S;
XX
XX WPI; 2001-662942/76.
DR N-PSDB; AAD21682.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1c11 heavy chain fragment which is used for the construction of chimeric
CC p1c11 IgG expression vector. Chimeric p1c11 heavy chain contains cloned
CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
CC domain (CH).
XX
SQ Sequence 136 AA;
Query Match 98.1%; Score 619; DB 22; Length 136;
Best Local Similarity 98.3%; Pred. No. 1.7e-46;
Matches 115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSY 60
Db 20 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSY 79
Qy 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGYEGYWGQTTVTSS 117
Db 80 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGYEGYWGQTTVTSS 136
RESULT 10
AAW28491
ID AAW28491 standard; Protein; 535 AA.
XX
AC AAW28491;
XX
DT 25-NOV-1997 (first entry)

XX Human p53 protein variant S-325 encoded by pEC176.

DE Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
XX substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX Chimeric - Homo sapiens.
OS Chimeric - Herpes simplex virus.
OS Synthetic.
XX WO9704092-A1.
XX 06-FEB-1997.
XX 17-JUL-1996; 96WO-FR01111.
XX 19-JUL-1995; 95FR-0008729.
XX (RHON) RHONE POULENC RORER SA.
XX Bracco L, Conseiller E;
XX WPI; 1997-132633/12.
XX N-PSDB; AAT86221.
XX New p53 variants e.g. with oligomerisation domain replaced by
PT leucine zipper - useful for treating hyper-proliferative disorders,
PT esp. cancer and restenosis
XX Claim 36; Pages 88-90; 133pp; French.
XX Claimed variants of protein p53 have at least part of the
CC oligomerisation domain deleted and replaced by a leucine zipper
CC domain. The mutants preferably also have at least part of the p53
CC transactivation domain (amino acids 1-74) deleted and replaced by
CC the transactivating domain (TD) from herpes simplex virus viral
CC protein VP16 (amino acids 411-490) or by a protein domain able to
CC bind selectively to a transactivator, especially a single-chain
CC antibody variable domain (ScFv). The present sequence is that of
CC a specifically claimed p53 variant designated S-325 and comprising
CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a
CC leucine zipper domain at the C-terminal. The p53 variants are
CC more active and more stable tumour suppressors and apoptosis-inducing
CC agents than wild-type p53 and are active where the wild-type protein
CC is not, i.e. they are not inactivated by dominant negative or oncogenic
CC mutants, nor by other cellular proteins (because the leucine zipper
CC domain prevents formation of inactive mixed oligomers).
XX
SQ Sequence 535 AA;
Query Match 88.5%; Score 558.5; DB 18; Length 535;
Best Local Similarity 88.9%; Pred. No. 1.3e-40;
Matches 104; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 3 QVQLQESGAELVSGASVKLSCTASGFNIKDYIMHVVKORPEQGLEWIGWIDPENGDT 62
QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSED TAVYYCNAYYGDYEGYWGQGT TTVVSS 117
Db 63 APKFQ GKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGT TTVVSS 118
RESULT 11
AAW28492
ID AAW28492 standard; Protein; 535 AA.
XX
AC AAW28492;
XX
DT 25-NOV-1997 (first entry)
XX

DE Human p53 protein variant S-325H.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX Chimeric - Homo sapiens.
OS Chimeric - Herpes simplex virus.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 361 /note= "Arg residue at position 182 of wild-type
FT p53 has been mutated to His"
FT
XX WO9704092-A1.
XX 06-FEB-1997.
XX 17-JUL-1996; 96WO-FR01111.
XX 19-JUL-1995; 95FR-0008729.
XX (RHON) RHONE POULENC RORER SA.
XX Bracco L, Conseiller E;
XX WPI; 1997-132633/12.
XX New p53 variants e.g. with oligomerisation domain replaced by
PT leucine zipper - useful for treating hyper-proliferative disorders,
PT esp. cancer and restenosis
XX Claim 36; Page -; 133pp; French.
XX Claimed variants of protein p53 have at least part of the
CC oligomerisation domain deleted and replaced by a leucine zipper
CC domain. The mutants preferably also have at least part of the p53
CC transactivation domain (amino acids 1-74) deleted and replaced by
CC the transactivating domain (TD) from herpes simplex virus viral
CC protein VP16 (amino acids 411-490) or by a protein domain able to
CC bind selectively to a transactivator, especially a single-chain
CC antibody variable domain (ScFv). The present sequence is that of
CC a specifically claimed p53 variant designated S-325H and comprising
CC a ScFv domain, amino acids 75-325 of human wild-type p53 (but with
CC Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
CC The p53 variants are more active and more stable tumour suppressors
CC and apoptosis-inducing agents than wild-type p53 and are active where
CC the wild-type protein is not, i.e. they are not inactivated by dominant
CC negative or oncogenic mutants, nor by other cellular proteins (because
CC the leucine zipper domain prevents formation of inactive mixed
CC oligomers).
CC (Note: this sequence does not appear in the specification and has
CC been produced by modifying the given sequence of variant V-325).
XX
SQ Sequence 535 AA;
Query Match 88.5%; Score 558.5; DB 18; Length 535;
Best Local Similarity 88.9%; Pred. No. 1.3e-40;
Matches 104; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 3 QVQLQESGAELVSGASVKLSCTASGFNIKDYIMHVVKORPEQGLEWIGWIDPENGDT 62
QY 61 APKFQ GKATMTADSSNTAYLQLSSLTSED TAVYYCNAYYGDYEGYWGQGT TTVVSS 117
Db 63 APKFQ GKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGT TTVVSS 118
RESULT 12
AAW70787

ID AAY70787 standard; Protein; 116 AA.
XX
AC AAY70787;
XX
DT 31-JUL-2000 (first entry)
XX
DE Murine anti-p53 monoclonal antibody PAb-421 heavy chain variable region.
XX
KW Murine; p53 protein; monoclonal antibody; PAb-421; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW heavy chain variable region; VH; complementarity determining region; CDR.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 26..35
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region 50..66
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region 99..105
FT /label= CDR
FT /note= "Complementarity determining region"
XX
PN WO200023082-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-US24443.
XX
PR 19-OCT-1998; 98US-0104816.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;
XX
DR WPI; 2000-339512/29.
XX
PT Treatment of systemic lupus erythematosus by down-regulating the
PT autoimmune response to the C-terminal DNA-binding domain of the p53
PT protein by an active compound comprising of antibodies to p53 or
PT fragments of p53 -
XX
PS Claim 78; Fig 9; 87pp; English.
XX
CC The patent discloses a method for the treatment of systemic lupus
CC erythematosus (SLE) by down-regulating the autoimmune response to the
CC C-terminal DNA-binding domain of p53 protein by an active compound.
CC The present sequence is a heavy chain variable region of monoclonal
CC antibody PAb-421 which is specific to the C-terminal DNA-binding domain
CC of murine p53 protein. PAb-421 antibody and peptides based on
CC complementarity determining regions of light and heavy chain variable
CC regions of the antibody, are examples of active compounds useful in the
CC diagnosis, prevention and treatment of SLE in humans.
XX
SQ Sequence 116 AA;
Query Match 87.9%; Score 554.5; DB 21; Length 116;
Best Local Similarity 88.9%; Pred. No. 5.8e-41;
Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
Db 1 QVKLQSGAELVSRGASVKLSCTASGFNKKDYMHVWKQRPQGLEWIGWIDPENGDTY 60
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQTTVTYSS 117
Db 61 APKFGKATMTADTSSNTAYLQLSSLASEDTAVYCN-FYGDALDYWGQTTVTYSS 116
RESULT 13

AAW60769
ID AAW60769 standard; Protein; 243 AA.
XX
AC AAW60769;
XX
DT 08-SEP-1998 (first entry)
XX
DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
XX
KW Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;
KW regulatory domain; p53 mutant; H273; W248; G281;
KW p53-dependent trans-activating activity; restoration;
KW tumour-suppressing activity; tumour cell; treatment;
KW hyper-proliferation; cancer; re-stenosis; ss.
XX
OS Mus sp.
XX
PN WO9818825-A1.
XX
PD 07-MAY-1998.
XX
PF 27-OCT-1997; 97WO-FR01921.
XX
PR 29-OCT-1996; 96FR-0013176.
XX
PA (RHON) RHONE-POULENC RORER SA.
XX
PI Debussche L, Bracco L;
XX
DR WPI; 1998-272140/24.
DR N-PSDB; AAV36236.
XX
PT Restoring p53-dependent trans-activating activity to cell containing
PT mutant p53 - by delivering single-chain antibody specific for the
PT mutant, particularly for treatment of tumours
XX
PS Claim 5; Page 31; 54pp; French.
XX
CC The present sequence represents a single chain antibody (ScFv) designated
CC 421. The antibody binds to an epitope present in the C-terminal region
CC of the p53 protein that includes oligomerisation and regulatory domains,
CC specifically between positions 320 and 393. ScFv 421 is directed against
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC introduced into cells containing a mutant p53 protein, p53-dependent
CC trans-activating activity is restored. ScFv 421 is specific for
CC p53-mutants that have lost tumour-suppressing activity and are present in
CC tumour cells. It is particularly used to treat hyper-proliferation
CC associated with these mutants (e.g. cancer and re-stenosis) but may also
CC be used in vitro for studying mechanisms of activity of p53 or its mutant
CC and to purify or detect p53.
XX
SQ Sequence 243 AA;
Query Match 87.7%; Score 553.5; DB 19; Length 243;
Best Local Similarity 88.9%; Pred. No. 1.5e-40;
Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
Db 1 QVKLQSGAELVSRGASVKLSCTASGFNKKDYMHVWKQRPQGLEWIGWIDPENGDTY 60
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQTTVTYSS 117
Db 61 APKFGKATMTADTSSNTAYLQLSSLASEDTAVYCN-FYGDALDYWGQTTVTYSS 116
RESULT 14
AAW89173
ID AAW89173 standard; peptide; 112 AA.
XX
AC AAW89173;
XX
DT 25-MAR-1999 (first entry)

XX Anti-p53 monoclonal antibody 421 variable heavy chain sequence.

DE

XX

KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;

KW immune response; tumour associated antigen; metastatic cancer.

XX

OS Mus sp.

OS Synthetic.

XX

PN WO9856416-A1.

XX

PD 17-DEC-1998.

XX

PF 09-JUN-1998; 98WO-IL00266.

XX

PR 09-JUN-1997; 97IL-0121041.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;

PI Wolkowicz R;

XX

DR WPI; 1999-070296/06.

XX

XX Use of a monoclonal antibody to a tumour-associated antigen - to

PT induce anti-tumour immunity or elicit an increased immune response

PT to the antigen

XX

PS Example 3; Fig 3; 47pp; English.

XX

CC The present invention describes the use of an immunogen (A) to induce

CC anti-tumour immunity; to elicit an increased immune response to tumour

CC associated antigen (TAA) and/or to induce an immune response to mutant

CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody

CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR

CC (complementarity determining region) on the heavy or light chain of Mab

CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the

CC variable (V) region of Mab, in a gene delivery vehicle. The present

CC sequence represents the variable heavy chain sequence from anti-p53 Mab

CC 421. Also described is a method for generating sequence-specific,

CC anti-DNA antibodies (Ab) by immunising a mammal with a Mab directed to a

CC domain containing a DNA-binding site of a DNA-binding protein. (A) is

CC used to treat a wide variety of primary and metastatic cancers,

CC particularly those where p53 is involved. Ab are used for diagnosis (e.g

CC to determine critical sequences in animal or plant breeding); to

CC identify bacteria and other parasites; to determine parentage; in

CC forensic science; to isolate specific genes for DNA vaccination; in gene

CC sequencing and cloning; also possibly for activation of selected

CC therapeutic genes in plants, animals and humans. (A) induce an effective

CC anti-tumour response without causing harm to the patient. The method

CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.

XX

SQ Sequence 112 AA;

Query Match 85.0%; Score 536.5; DB 20; Length 112;

Best Local Similarity 88.5%; Pred. No. 2.1e-39;

Matches 100; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 4 LQSGAELVSGASVKLSCTTSGFNKDFYMHVVKQRPEQGLEWIDPENGDSYAPK 63

||:||||| |||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 1 LQESGAELVRSGASVKLSCTASGFNIKDYMHVVKQRPEQGLEWIDPENGDTYAPK 60

QY 64 FQKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQTTVTS 116

|||||||:||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 61 FQKATMTADTSSNTAYLQLSSLASEDTAVYCN-FYGDALDYWGQTTVTS 112

RESULT 15

AAW01586

ID AAW01586 standard; Protein; 118 AA.

XX

AC AAW01586;

XX

DT 22-AUG-1997 (first entry)

XX

DE Lead binding MAb 14G11 heavy chain variable region.

XX

KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;

KW pharmaceutical; health care; skin treatment; pesticide; herbicide;

KW heavy metal.

XX

OS Mus musculus.

XX

PN WO9639518-A1.

XX

PD 12-DEC-1996.

XX

PF 05-JUN-1996; 96WO-US09258.

XX

PR 10-OCT-1995; 95US-0541373.

PR 05-JUN-1995; 95US-0462798.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Lopez O, Murray PJ, Wylie DE;

XX

DR WPI; 1997-043140/04.

DR N-PSDB; AAT58260.

XX

PT DNA encoding heavy metal binding polypeptide sequences - used for

PT detecting, removing, adding or neutralising heavy metals, such as

PT lead cations

XX

PS Claim 12; Page 75; 125pp; English.

XX

CC The present sequence represents the heavy chain variable region for

CC monoclonal antibody (Mab) 14G11, which immunoreacts with a lead cation.

CC The sequence was derived from RNA isolated from mouse hybridoma cells.

CC The protein can be used for binding heavy metals, such as lead cations.

CC It can be used for detecting, removing, adding or neutralising the

CC heavy metals in biological and inanimate systems. It can be used in

CC e.g. aqueous liquid systems, in biological or environmental systems or

CC in such compositions as perfumes, cosmetics, pharmaceuticals, health

CC care products, skin treatment products, pesticides, herbicides,

CC solvents used in the production of semi-conductor and integrated

CC circuit components and production materials for electronic components.

CC The products can provide for applications involving minute amounts of

CC specific heavy metals.

XX

SQ Sequence 118 AA;

Query Match 85.0%; Score 536.5; DB 18; Length 118;

Best Local Similarity 85.6%; Pred. No. 2.2e-39;

Matches 101; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVVKQRPEQGLEWIDPENGDSY 60

:|:||||||| |||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYMHVVKQRPEQGLEWIDPENGDTY 60

QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDYAVYCNAY-YGDYEGYWGQTTVTSS 117

|||||||:||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 61 DPKFQKATMTADTSSNIAYLQLSSLTSEDYAVYCNPYGYDDAMDYWGQTSVTSS 118

Search completed: December 23, 2002, 07:25:10

Job time : 63.8081 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 56.9031 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-23
Perfect score: 549
Sequence: 1 DIELTQSPAIMSASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	AAE13144	Humanised antibody
2	549	100.0	106	AAU74418	Antigen-binding pr
3	549	100.0	108	AAU97236	Variable light cha
4	549	100.0	108	AAU82710	VEGF antagonist an
5	549	100.0	108	AAU74413	Antigen-binding pr
6	549	100.0	125	AAE13146	Chimeric pIC11 lig
7	549	100.0	125	AAU82702	VEGF antagonist an
8	549	100.0	238	AAU74420	Antigen-binding pr
9	549	100.0	240	AAU74419	Antigen-binding pr
10	549	100.0	330	AAU70842	SNV-env leader/hum

11	534	97.3	108	16	AAU79884	Anti-EGFR antibody
12	534	97.3	235	18	AAU41392	Chimeric anti-CEA
13	532	96.9	108	13	AAU21290	Murine VL kappa gr
14	532	96.9	108	18	AAU41388	Anti-CEA antibody
15	529	96.4	107	22	AAU83159	Mouse ganglioside
16	529	96.4	129	15	AAU53329	KM-796 and KM-750
17	529	96.4	129	20	AAU28385	Anti-GM2 light cha
18	529	96.4	129	20	AAU28357	Antibody chain use
19	527	96.0	256	22	AAU82897	Anti-p53 common mu
20	527	96.0	258	22	AAU82898	Anti-p53 common mu
21	526	95.8	107	22	AAU63987	Amino acid sequenc
22	524	95.4	108	13	AAU21294	Murine VL kappa gr
23	523	95.3	236	20	AAU34096	Partial amino acid
24	523	95.3	270	16	AAU75719	MFE-23 antibody.
25	523	95.3	553	18	AAU11508	Single chain anti-
26	523	95.3	553	20	AAU73223	H22-anti-CEA antib
27	523	95.3	553	22	AAU85455	Bispecific single
28	523	95.3	553	22	AAU61960	Bispecific single
29	521	94.9	281	20	AAU82744	Fusion protein pIC
30	521	94.9	666	20	AAU82745	Fusion protein (80
31	519	94.5	109	23	AAU81278	Murine trkC antibo
32	519	94.5	556	22	AAU97935	scFv-rearranged ca
33	519	94.5	556	22	AAU80040	scFv-rearranged ca
34	518	94.4	105	17	AAU03182	Guy's 13 anti-Stre
35	516	94.0	106	13	AAU24105	Anti-Tac light cha
36	516	94.0	106	19	AAU58511	Protein SEQ ID NO:
37	516	94.0	106	22	AAU69641	Murine anti-Tac an
38	516	94.0	106	22	AAU69651	Murine anti-Tac an
39	516	94.0	128	10	AAU93150	Protein encoded by
40	516	94.0	239	21	AAU12563	Anti-TAC scFv prote
41	516	94.0	239	22	AAU36826	Anti-TAC scFv prote
42	516	94.0	599	19	AAU37132	Anti-Tac(Fv)-PE40
43	516	94.0	599	20	AAU95462	Anti-Tac(Fv)-PE40
44	516	94.0	599	21	AAU87477	Anti-Tac(Fv)-PE40
45	511	93.1	128	21	AAU19639	Mouse monoclonal a

ALIGNMENTS

RESULT 1
AAE13144
ID AAE13144 standard; Protein; 106 AA.

AC	AAE13144;				
XX					
DT	28-JAN-2002	(first entry)			
DE	Humanised antibody	light chain	fragment.		
XX					
KW	Vascular endothelial	growth factor	receptor; VEGFR; antagonist; tumour;		
KW	cytostatic; light	chain; myelocytic	leukaemia; lymphocytic; erythrocytic;		
KW	monocytic; multiple	myeloma; lymphoid	cell; Hodgkin's disease; mouse;		
KW	human; chimeric.				
XX					
OS	Chimeric - Homo sapiens.				
OS	Chimeric - Mus sp.				
XX					
PN	WO200174296-A2.				
XX					
PD	11-OCT-2001.				
XX					
PF	30-MAR-2001; 2001WO-US10504.				
XX					
PR	31-MAR-2000; 2000US-0540770.				
XX					
PA	(IMCL-) IMCLONE SYSTEMS INC.				
PA	(CORR) CORNELL RES FOUND INC.				
XX					
PI	Witte L, Rafii S;				
XX					
DR	WPI; 2001-662942/76.				
DR	N-PSDB; AAD21670.				

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 16; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody light chain fragment used in the exemplification of the
XX invention.

SQ Sequence 106 AA;
Query Match 100.0%; Score 549; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
|||
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106

RESULT 2
AAU74418
ID AAU74418 standard; peptide; 106 AA.
XX
AC AAU74418;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein light chain variable domain (VH) #2.
XX
KW Antigen-binding protein; antibody light chain variable domain;
KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp
XX
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAU20289.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -

PS Claim 61; Page 61; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a light chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.

XX Sequence 106 AA;
SQ

Query Match 100.0%; Score 549; DB 23; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
|||
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
|||
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106

RESULT 3
AAU97236
ID AAU97236 standard; Protein; 108 AA.
XX
AC AAU97236;
XX
DT 19-DEC-2000 (first entry)
XX
DE Variable light chain fragment of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX

PI Zhu Z, Witte L;
XX
DR WPI; 2000-505966/45.
DR N-PSDB; AAA53768.
XX
PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 4; Page 51; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 549; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMASPGKEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMASPGKEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
RESULT 4
AAB82710
ID AAB82710 standard; Protein; 108 AA.
XX
AC AAB82710;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 light chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24..33
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT 49..55
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT 88..96
FT /label= CDR-L3
FT /note= "complementarity determining region 3"
XX

PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26406.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent
XX
PS Disclosure; Page 38-39; 42pp; English.
XX
CC The present sequence is that of the light chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC ovarian carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 549; DB 22; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMASPGKEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMASPGKEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
RESULT 5
AAU74413
ID AAU74413 standard; peptide; 108 AA.
XX
AC AAU74413;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein light chain variable domain (VH) #1.
XX
KW Antigen-binding protein; antibody light chain variable domain;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.

XX Mus sp.
OS WO200190192-A2.
XX
PN
XX
PD 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
PF
PR 24-MAY-2000; 2000US-206749P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20284.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 57; Page 57; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a light chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 549; DB 23; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMASASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60

QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 6
AAE13146
ID AAE13146 standard; Protein; 125 AA.
XX
AC AAE13146;
XX
XX 28-JAN-2002 (first entry)
DT
XX Chimeric p1C11 light chain fragment.
DE
XX

KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human; p1C11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Leader_peptide
FT Protein 20..125
FT /note= "Mature chimeric p1C11 light chain fragment"
FT Region 43..52
FT /label= CDR_L1
FT Region 68..74 /label= CDR_L2
FT Region 107..115 /label= CDR_L3
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10504.
PF
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafil S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21683.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1C11 light chain fragment which is used for the construction of chimeric
CC p1C11 IgG expression vector. Chimeric p1C11 light chain contains cloned
CC variable light chain (VL) and human kappa light chain constant region
CC (CL).
XX
SQ Sequence 125 AA;

Query Match 100.0%; Score 549; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.6e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
DB 20 DIELTQSPAIMASASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 79

QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 80 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 7
AAB82702
ID AAB82702 standard; Protein; 125 AA.
XX
AC AAB82702;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 light chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..125
FT /label= Mature_protein
FT Region 43..52
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT Region 68..74
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT Region 107..115
FT /label= CDR-L3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAB26414.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
PS Disclosure; Fig 1; 42pp; English.
XX
CC The present sequence is that of the light chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,

CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 125 AA;

Query Match 100.0%; Score 549; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.6e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
DB 20 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 79
QY 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 80 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 8
AAU74420
ID AAU74420 standard; Protein; 238 AA.
XX
AC AAU74420;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #2.
XX
KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 61"
FT Region 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable fragment
FT protein. Encoded by AAS20285"
FT Region 133..238
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 61"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX

PS Claim 63; Page 62-63; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

CC light chain constant domain (CL domain), and P2 has an antigen-binding

CC site located to the N terminus of a CH1 domain. (I) is useful for:

CC neutralising the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This is the amino acid sequence of a single chain variable fragment

CC (scFv), an engineered protein containing a variable light and variable

CC heavy domain on one polypeptide, described in the method of the

CC invention.

XX

SQ Sequence 238 AA;

Query Match 100.0%; Score 549; DB 23; Length 238;

Best Local Similarity 100.0%; Pred. No. 1.2e-31;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60

Db 133 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 192

QY 61 FSGSGSGTSYSLTISRMEADAATYCCQRRSSYPFTFGSGTKLEIK 106

Db 193 FSGSGSGTSYSLTISRMEADAATYCCQRRSSYPFTFGSGTKLEIK 238

RESULT 9

AAU74419

ID AAU74419 standard; Protein; 240 AA.

XX

AC AAU74419;

XX

DT 26-MAR-2002 (first entry)

XX

DE Antigen-binding protein, single chain variable fragment version #1.

XX

KW Antigen-binding protein; single chain variable fragment; scFv; antigen;

KW cytotostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.

XX

OS Mus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 1..117

FT /label= VH

FT /note= "Heavy chain variable domain. Specifically

FT claimed in claim 57"

FT

FT 118..132

FT /label= Linker

FT /note= "15 amino acid linker joins the VH and VL

FT regions of the single chain variable

FT fragment protein. Encoded by AAS20285"

FT

FT 133..240

FT /label= VL

FT /note= "Light chain variable domain. Specifically

FT claimed in claim 57"

FT

XX WO200190192-A2.

PN

XX

PD 29-NOV-2001.

XX

PF 24-MAY-2001; 2001WO-US16924.

XX

PR 24-MAY-2000; 2000US-206749P.

XX

PA (IMCL-) IMCLONE SYSTEMS INC.

XX

PI Zhu Z;

XX

DR WPI; 2002-106189/14.

XX

PT New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX

PS Claim 63; Page 62; 64pp; English.

XX

CC The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

CC light chain constant domain (CL domain), and P2 has an antigen-binding

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC neutralising the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This is the amino acid sequence of a single chain variable fragment

CC (scFv), an engineered protein containing a variable light and variable

CC heavy domain on one polypeptide, described in the method of the

CC invention.

XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 549; DB 23; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.2e-31;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60

Db 133 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 192

QY 61 FSGSGSGTSYSLTISRMEADAATYCCQRRSSYPFTFGSGTKLEIK 106

Db 193 FSGSGSGTSYSLTISRMEADAATYCCQRRSSYPFTFGSGTKLEIK 238

RESULT 10

AAB70842

ID AAB70842 standard; Protein; 330 AA.

XX

AC AAB70842;

XX

DT 25-JUN-2001 (first entry)

XX

DE SNV-env leader/human 7B2-scFv fusion construct.

XX

KW T lymphocyte; antibody; single chain variable antibody; scFv; human;

KW cell-targeting vector; antiviral; cytotostatic; immunostimulant; AIDS;

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;

Db 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 106
RESULT 14
AAW41388
ID AAW41388 standard; Protein; 108 AA.
XX AC AAW41388;
XX DT 02-JUN-1998 (first entry)
XX DE Anti-CEA antibody 806.077 light chain variable region.
XX KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region; light chain.
XX OS Synthetic.
XX PN WO9742329-A1.
XX PD 13-NOV-1997.
XX PF 29-APR-1997; 97WO-GB01165.
XX PR 14-FEB-1997; 97GB-0003103.
XX PR 04-MAY-1996; 96GB-0009405.
XX PA (ZENE) ZENECA LTD.
XX PI Copley CG, Edge MD, Emery SC;
XX WPI; 1997-558987/51.
XX DR N-PSDB; AAV17270.
XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
diagnosis and therapy of cancer
XX PS Claim 3; Page 196; 208pp; English.
XX CC This sequence is the light chain variable region of the antibody of
the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
antibody (806.077 Ab). Host cells or transgenic organisms transformed
with DNA encoding the antibody, are used to make the antibody or
conjugate. The conjugate is used in a medicament suitable for intravenous
administration. The conjugate can be used for cancer therapy, selectively
killing tumour cells. The antibody can be used for in vivo or in vitro
diagnosis of cancer.
XX SQ Sequence 108 AA;
Query Match 96.9%; Score 532; DB 18; Length 108;
Best Local Similarity 95.3%; Pred. No. 9.2e-31;
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMASPGKVTITCSASSSVTYMHWFQKPGTSPKLIYSTSNLASGVPAR 60
QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 106
Db 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPPLTFGAGTKLEIK 106
RESULT 15
AAB83159
ID AAB83159 standard; protein; 107 AA.
XX AC AAB83159;
XX DT 02-JUL-2001 (first entry)
XX DE Mouse ganglioside GM2 antibody-related protein #2.

XX Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX Mus sp.
XX WO200123431-A1.
XX PD 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-JP06775.
XX PR 30-SEP-1999; 99JP-0278292.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Nakamura K, Niwa R;
XX DR WPI; 2001-266142/27.
XX PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
PT radioisotopes or proteins for treatment and diagnosis of cancer -
XX PS Claim 29; Page 69-70; 80pp; Japanese.
XX CC The present invention relates to derivatives of an antibody against
ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope,
CC protein or small drug in the treatment and diagnosis of cancer.
XX SQ Sequence 107 AA;
Query Match 96.4%; Score 529; DB 22; Length 107;
Best Local Similarity 97.1%; Pred. No. 1.5e-30;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPARF 61
Db 2 IVLTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIYSTSNLASGVPARF 61
QY 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 106
Db 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGGGTKLEIK 106
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Job time : 56.9031 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 1.5814 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDYAPKFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	10	US-09-976-787-22 Sequence 22, Appl
2	101	100.0	17	10	US-09-865-198-21 Sequence 21, Appl
3	101	100.0	117	10	US-09-976-787-23 Sequence 23, Appl
4	101	100.0	117	10	US-09-865-198-22 Sequence 22, Appl
5	101	100.0	238	10	US-09-976-787-29 Sequence 29, Appl
6	101	100.0	238	10	US-09-865-198-28 Sequence 28, Appl
7	94	93.1	17	10	US-09-976-787-2 Sequence 2, Appli
8	94	93.1	17	10	US-09-865-198-2 Sequence 2, Appli
9	94	93.1	117	10	US-09-976-787-7 Sequence 7, Appli
10	94	93.1	117	10	US-09-865-198-7 Sequence 7, Appli
11	94	93.1	124	9	US-09-974-052-1 Sequence 1, Appli
12	94	93.1	124	9	US-09-974-052-3 Sequence 3, Appli
13	94	93.1	124	9	US-09-974-052-4 Sequence 4, Appli
14	94	93.1	124	9	US-09-974-052-5 Sequence 5, Appli
15	94	93.1	124	9	US-09-974-052-6 Sequence 6, Appli
16	94	93.1	124	9	US-09-974-052-7 Sequence 7, Appli
17	94	93.1	124	9	US-09-974-052-8 Sequence 8, Appli
18	94	93.1	124	9	US-09-974-052-9 Sequence 9, Appli
19	94	93.1	124	9	US-09-974-052-10 Sequence 10, Appl

20	94	93.1	124	9	US-09-974-052-11	Sequence 11, Appl
21	94	93.1	124	9	US-09-974-052-12	Sequence 12, Appl
22	94	93.1	124	9	US-09-974-051-1	Sequence 1, Appli
23	94	93.1	124	9	US-09-974-051-3	Sequence 3, Appli
24	94	93.1	124	9	US-09-974-051-4	Sequence 4, Appli
25	94	93.1	124	9	US-09-974-051-5	Sequence 5, Appli
26	94	93.1	124	9	US-09-974-051-6	Sequence 6, Appli
27	94	93.1	124	9	US-09-974-051-7	Sequence 7, Appli
28	94	93.1	124	9	US-09-974-051-8	Sequence 8, Appli
29	94	93.1	124	9	US-09-974-051-9	Sequence 9, Appli
30	94	93.1	124	9	US-09-974-051-10	Sequence 10, Appl
31	94	93.1	124	9	US-09-974-051-11	Sequence 11, Appl
32	94	93.1	124	9	US-09-974-051-12	Sequence 12, Appl
33	94	93.1	240	10	US-09-976-787-28	Sequence 28, Appl
34	94	93.1	240	10	US-09-865-198-27	Sequence 27, Appl
35	90	89.1	17	10	US-09-910-059-31	Sequence 31, Appl
36	90	89.1	120	10	US-09-910-059-11	Sequence 11, Appl
37	90	89.1	120	10	US-09-910-059-55	Sequence 55, Appl
38	90	89.1	120	10	US-09-910-059-75	Sequence 75, Appl
39	90	89.1	120	10	US-09-910-059-79	Sequence 79, Appl
40	90	89.1	120	10	US-09-910-059-81	Sequence 81, Appl
41	90	89.1	120	10	US-09-910-059-85	Sequence 85, Appl
42	90	89.1	120	10	US-09-910-059-89	Sequence 89, Appl
43	90	89.1	120	10	US-09-910-059-91	Sequence 91, Appl
44	90	89.1	255	10	US-09-910-059-19	Sequence 19, Appl
45	90	89.1	255	10	US-09-910-059-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-22
; Sequence 22, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-22

Query Match 100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQG 17
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Db 1 WIDPENGSDYAPKFQG 17

RESULT 2
US-09-865-198-21
; Sequence 21, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-21

Query Match 100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||

Db 1 WIDPENGSDYAPKFQ 17

RESULT 3
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||

Db 50 WIDPENGSDYAPKFQ 66

RESULT 4
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||

Db 50 WIDPENGSDYAPKFQ 66

RESULT 5
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 101; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||

Db 50 WIDPENGSDYAPKFQ 66

RESULT 6
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 101; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||

Db 50 WIDPENGSDYAPKFQ 66

RESULT 7
US-09-976-787-2

; Sequence 2, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-2

Query Match 93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||
Db 1 WIDPENGDSGYAPKFQ 17

RESULT 8

US-09-865-198-2
; Sequence 2, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2

Query Match 93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||
Db 1 WIDPENGDSGYAPKFQ 17

RESULT 9

US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match 93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 9.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||
Db 50 WIDPENGDSGYAPKFQ 66

RESULT 10

US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

Query Match 93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 9.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFQ 17
|||||
Db 50 WIDPENGDSGYAPKFQ 66

RESULT 11

US-09-974-052-1
; Sequence 1, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124


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; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-052-1
Query Match 93.1%; Score 94; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 1e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFAQ 17
Db 50 WIDPENGDTYAPKFAQ 66

RESULT 12
US-09-974-052-3
; Sequence 3, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-3
Query Match 93.1%; Score 94; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 1e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFAQ 17
Db 50 WIDPENGDTYAPKFAQ 66

RESULT 14
US-09-974-052-5
; Sequence 5, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-5
Query Match 93.1%; Score 94; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 1e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFAQ 17
Db 50 WIDPENGDTYAPKFAQ 66

RESULT 13
US-09-974-052-4
; Sequence 4, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
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; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 4
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-4
Query Match 93.1%; Score 94; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 1e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFAQ 17
Db 50 WIDPENGDTYAPKFAQ 66

RESULT 14
US-09-974-052-5
; Sequence 5, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-974-052-5
Query Match 93.1%; Score 94; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 1e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFAQ 17
Db 50 WIDPENGDTYAPKFAQ 66

RESULT 15
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OM protein - protein search, using sw model

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(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-8
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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
Maximum Match 100%
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	100.0	108	21	Variable light cha
2	558	100.0	108	22	VEGF antagonist an
3	558	100.0	108	23	Antigen-binding pr
4	558	100.0	240	23	Antigen-binding pr
5	558	100.0	330	22	SNV-env leader/hum
6	549	98.4	106	22	Humanised antibody
7	549	98.4	106	23	Antigen-binding pr
8	549	98.4	125	22	Chimeric p1C11 lig
9	549	98.4	125	22	VEGF antagonist an
10	549	98.4	238	23	Antigen-binding pr

11	543	97.3	108	16	AAR79884	Anti-EGFR antibody
12	541	97.0	108	13	AAR21290	Murine VL kappa gr
13	541	97.0	108	18	AAW41388	Anti-CEA antibody
14	539	96.6	235	18	AAW41392	Chimeric anti-CEA
15	536	96.1	256	22	AAB82897	Anti-p53 common mu
16	536	96.1	258	22	AAB82898	Anti-p53 common mu
17	534	95.7	107	22	AAB83159	Mouse ganglioside
18	534	95.7	129	15	AAR53329	KM-796 and KM-750
19	534	95.7	129	20	AAV28385	Anti-GM2 light cha
20	534	95.7	129	20	AAV28357	Antibody chain use
21	533	95.5	108	13	AAR21294	Murine VL kappa gr
22	532	95.3	270	16	AAR75719	MFE-23 antibody.
23	532	95.3	553	18	AAW11508	Single chain anti-
24	532	95.3	553	20	AAW73223	H22-anti-CEA antib
25	532	95.3	553	22	AAB85455	Bispecific single
26	532	95.3	553	22	AAB61960	Bispecific single
27	531	95.2	107	22	AAG63987	Amino acid sequenc
28	528	94.6	236	20	AAV34096	Partial amino acid
29	526	94.3	281	20	AAW82744	Fusion protein pIC
30	526	94.3	666	20	AAW82745	Fusion protein (80
31	524	93.9	109	23	AAU81278	Murine trkC antibo
32	519	93.0	556	22	AAU97935	scFv-rearranged ca
33	519	93.0	556	22	AAU80040	scFv-rearranged ca
34	518	92.8	105	17	AAW03182	Guy's 13 anti-Stre
35	516	92.5	106	13	AAR24105	Anti-Tac light cha
36	516	92.5	106	19	AAW58511	Protein SEQ ID NO:
37	516	92.5	106	22	AAB69641	Murine anti-Tac an
38	516	92.5	106	22	AAB69651	Murine anti-Tac an
39	516	92.5	128	10	AAV93150	Protein encoded by
40	516	92.5	239	21	AAAB12563	Anti-TAC sfv prote
41	516	92.5	239	22	AAB36826	Anti-TAC sfv prote
42	516	92.5	599	19	AAW37132	Anti-Tac(Fv)-PE40
43	516	92.5	599	20	AAW95462	Anti-Tac(Fv)-PE40
44	516	92.5	599	21	AAV87477	Anti-Tac(Fv)-PE40
45	511	91.6	128	21	AAB19639	Mouse monoclonal a

ALIGNMENTS

RESULT 1

AAV97236

ID AAV97236 standard; Protein; 108 AA.

XX AAV97236;

XX 19-DEC-2000 (first entry)

DT Variable light chain fragment of anti-SI(KDR) antibody.

DE Immunoglobulin; antibody; complementary determining region; CDR;

DE VEGF; vascular endothelial growth factor; KDR;

KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diabody; triabody;

KW glioblastoma multiforme; hemangioblastoma; AIDS;

KW central nervous system neoplasms; AIDS associated Karposi's sarcoma;

KW acquired immune deficiency syndrome; AIDS; human.

XX Homo sapiens.

OS Synthetic.

XX WO200044777-A1.

XX 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US02180.

XX 29-JAN-1999; 99US-0117726.

PR 29-JAN-1999; 99US-0240736.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z, Witte L;

PI

Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 192
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
Db 193 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 240

RESULT 5
AAB70842
ID AAB70842 standard; Protein; 330 AA.
XX
AC AAB70842;
XX
DT 25-JUN-2001 (first entry)
XX
DE SNV-env leader/human 7B2-scfv fusion construct.
XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Spleen necrosis virus.
XX
FH Key Location/Qualifiers
FT Protein 1..45
FT /label= SNV-env_leader
FT 46..330
FT /label= 7B2-scfv
XX
PN DE19946142-A1.
XX
PD 29-MAR-2001.
XX
PF 27-SEP-1999; 99DE-1046142.
XX
PR 27-SEP-1999; 99DE-1046142.
XX
PA (BUND)-BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
PI Cichutek K, Engelstaedter M;
XX
DR WPI; 2001-246140/26.
DR N-PSDB; AAF61511.
XX
PT Cell-targeting vector selective for T lymphocytes, useful in gene
PT therapy of e.g. acquired immune deficiency syndrome, encodes a
PT single-chain variable antibody fragment .
XX
PS Claim 1; Fig 3; 18pp; German.
XX
CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human/B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with x-gal to
CC determine transfection. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 7B2-scfv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.

XX
SQ Sequence 330 AA;
Query Match 100.0%; Score 558; DB 22; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
Db 181 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 240
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
Db 241 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 288

RESULT 6
AAE13144
ID AAE13144 standard; Protein; 106 AA.
XX
AC AAE13144;
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody light chain fragment.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafii S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21670.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 16; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody light chain fragment used in the exemplification of the
XX
SQ Sequence 106 AA;

CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1c11 light chain fragment which is used for the construction of chimeric
CC p1c11 IgG expression vector. Chimeric p1c11 light chain contains cloned
CC variable light chain (VL) and human kappa light chain constant region
CC (CL).

XX Sequence 125 AA;

Query Match 98.4%; Score 549; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.2e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSGVPAR 60
Db 20 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSGVPAR 79
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 80 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 9
AAB82702
ID AAB82702 standard; Protein; 125 AA.

XX AAB82702;

DT 15-OCT-2001 (first entry)

DE VEGF antagonist antibody IMC-1c11 light chain variable region.

XX IMC-1c11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.

OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..125
FT /label= Mature_protein
FT Region 43..52
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT Region 58..74
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT Region 107..115
FT /label= CDR-L3
FT /note= "complementarity determining region 3"

XX WO200154723-A1.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US02839.

XX 28-JAN-2000; 2000US-0178791.

XX 31-MAR-2000; 2000US-0539692.

PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.

PA (IMCL-) IMCLONE SYSTEMS INC.

XX Kerbel R;

XX WPI; 2001-514531/56.

XX N-PSDB; AAH26414.

XX Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent

XX Disclosure; Fig 1; 42pp; English.

XX The present sequence is that of the light chain variable region of
CC IMC-1c11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1c11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

SQ Sequence 125 AA;

Query Match 98.4%; Score 549; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.2e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSGVPAR 60
Db 20 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSGVPAR 79
QY 61 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 80 FSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 10
AAU74420
ID AAU74420 standard; Protein; 238 AA.

XX AAU74420;

XX 26-MAR-2002 (first entry)

XX Antigen-binding protein, single chain variable fragment version #2.
KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.

OS Mus sp.
OS Synthetic.

XX Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 61"

FT Region 118..132

FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable fragment
FT protein. Encoded by AAS20285"
FT 133..238
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 61"
XX
PN WO200190192-A2.
XX
XX 29-NOV-2001.
PD
XX 24-MAY-2001; 2001WO-US16924.
PF
XX 24-MAY-2000; 2000US-206749P.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 63; Page 62-63; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
XX invention.
SQ Sequence 238 AA;
Query Match 98.4%; Score 549; DB 23; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.6e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 192
QY 61 FSGSGSGTYSYSLTISRMEAEADAATYCCQRRSSYPFTFGSGTKLEIK 106
Db 193 FSGSGSGTYSYSLTISRMEAEADAATYCCQRRSSYPFTFGSGTKLEIK 238
RESULT 11
AAR79884
ID AAR79884 standard; Protein; 108 AA.
XX
AC AAR79884;

XX 02-JUL-1996 (first entry)
DT
XX
DE Anti-EGFR antibody light chain variable region (Clone L2 8C).
XX
KW Single chain antibody; antibody; epidermal growth factor receptor;
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
KW assessment; phage antibody library.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..23 /label= Framework region 1.
FT Region 24..33 /label= CDR1.
FT Region 34..48 /label= CDR2.
FT Region 49..55 /label= CDR2.
FT Region 56..87 /label= Framework region 3.
FT Region 88..96 /label= CDR3.
FT Region 97..108 /label= CDR3.
FT Region 97..108 /label= Framework region 4.
XX
PN WO9525167-A1.
XX
PD 21-SEP-1995.
XX
PF 16-MAR-1995; 95WO-EP00978.
XX
PR 02-DEC-1994; 94EP-0118970.
PR 17-MAR-1994; 94EP-0104160.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Adan J, Ansell KH, Bendig MM, Blasco F, Gussow D;
PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;
XX
DR WPI; 1995-336972/43.
XX
PT Anti-EGFR antibodies and single chain Fv antibody fragments -
PT obtained from phage-antibody libraries, useful for diagnosis and
PT therapy of tumours
XX
PS Disclosure: Figure 1A; 93pp; English.
XX
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC and antibodies constructed from anti-EGFR antibody fragments can be
CC used for diagnosis of tumours and assessment of tumour growth in
CC vitro and in vivo. They may also be used in a pharmaceutical
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC The antibodies and fragments are derived from mice but are humanised
CC so as to cause minimum reaction against them. They are produced
CC using the phage antibody library.
XX
SQ Sequence 108 AA;
Query Match 97.3%; Score 543; DB 16; Length 108;
Best Local Similarity 96.3%; Pred. No. 2.1e-31;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTYSYSLTISRMEAEADAATYCCQRRSSYPFTFGSGTKLEIKRA 108
Db 61 FSGSGSGTYSYSLTISRMEAEADAATYCCQRRSSYPHTFGAGTKLEIKRA 108

RESULT 12
AAR21290
ID AAR21290 standard; Protein; 108 AA.
XX
AC AAR21290;
XX
DT 21-MAY-1992 (first entry)
XX
DE Murine VL kappa group VI chain "e", specific for phOx.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Binding-site 24..33
FT /label= CDR1
FT Binding-site 49..55
FT /label= CDR2
FT Binding-site 88..96
FT /label= CDR3
FT /note=" D-X-G-X-X motif "
XX
PN WO9201047-A.
XX
PD 23-JAN-1992.
XX
PF 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter JGP, Bonner TP;
XX
DR WPI; 1992-056862/07.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 21; Fig 24; 209pp; English.
XX
CC The V_L sequence is one of seven (AAR21286-92) found to be expressed
CC from a single chain Fv library from an immunised mouse. The libra-
CC ry produces a diverse repertoire of antibody fragments specific for
CC 2-phenyl-5-oxazolone (phOx). It was prepd. using cDNA generated
CC from mRNA from mice immunised with phOx coupled to chicked serum
CC albumin. The VH and VL kappa sequences were separately amplified
CC by PCR (see AAQ23474-84) and ligated into fdCAT2 (see AAQ23463) for ex-
CC pression on the phage surface as fusions with gene III. The result-
CC ing library of clones was diverse. Twenty three haptens binding
CC clones were sequenced revealing eight different VH genes (A-H) (see
CC AAR21264-71) in a variety of pairings with the seven different V_L
CC genes (a-g). Of the twenty three clones sequenced, four were of
CC type "e", and were "ox-like" genes. (See Berek et al, Nature 316
CC 412-418, 1985). They contain the DXGX motif in CDR3, the central
CC Gly of which is needed to create a cavity for phOx. Most of the
CC clones were V_L-d combinations. The Kd of V_H-B/V_L-b for phOx-GABA
CC was 10 uM, one of the highest values found. This suggests that
CC phage bearing scFv fragments having weak affinities can be selected
CC with antigen, probably due to the avidity of the multiple antibody
CC heads on the phage.
CC See also AAR21260-307, 309-311; AAR22450, 565-581.

XX
SQ Sequence 108 AA;
Query Match 97.0%; Score 541; DB 13; Length 108;
Best Local Similarity 97.2%; Pred. No. 3e-31;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSPGKVKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMSPGKVKVTITCSASSSVNYMHWFQKPGTSPKLIWYSTSNLASGVPTR 60
QY 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPPTFGSGTKLEIKRA 108
DB 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPPTFGSGTKLEIKRA 108
RESULT 13
AAW41388
ID AAW41388 standard; Protein; 108 AA.
XX
AC AAW41388;
XX
DT 02-JUN-1998 (first entry)
XX
DE Anti-CEA antibody 806.077 light chain variable region.
XX
KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region; light chain.
XX
OS Synthetic.
XX
PN WO9742329-A1.
XX
PD 13-NOV-1997.
XX
PF 29-APR-1997; 97WO-GB01165.
XX
PR 14-FEB-1997; 97GB-0003103.
PR 04-MAY-1996; 96GB-0009405.
XX
PA (ZENÉ) ZENECA LTD.
XX
PI Copley CG, Edge MD, Emery SC;
XX
DR WPI; 1997-558987/51.
DR N-PSDB; AAV17270.
XX
PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
PT diagnosis and therapy of cancer
XX
PS Claim 3; Page 196; 208pp; English.
XX
CC This sequence is the light chain variable region of the antibody of
CC the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
CC with DNA encoding the antibody, are used to make the antibody or
CC conjugate. The conjugate is used in a medicament suitable for intravenous
CC administration. The conjugate can be used for cancer therapy, selectively
CC killing tumour cells. The antibody can be used for in vivo or in vitro
CC diagnosis of cancer.
XX
SQ Sequence 108 AA;
Query Match 97.0%; Score 541; DB 18; Length 108;
Best Local Similarity 95.4%; Pred. No. 3e-31;
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSPGKVKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMSPGKVKVTITCSASSSVTYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPPTFGSGTKLEIKRA 108
|||||

Db 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSTYPLTFGAGTKLELKRA 108

RESULT 14

AAW41392

ID AAW41392 standard; Protein; 235 AA.

XX AAW41392;

XX 02-JUN-1998 (first entry)

XX Chimeric anti-CEA antibody 806.077 light chain.

DT Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
DE cancer diagnosis; complementarity determining region; light chain.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX WO9742329-A1.

PN 13-NOV-1997.

XX 29-APR-1997; 97WO-GB01165.

XX 14-FEB-1997; 97GB-0003103.

PR 04-MAY-1996; 96GB-0009405.

XX (ZENE) ZENECA LTD.

XX Copley CG, Edge MD, Emery SC;

XX WPI; 1997-558987/51.

DR N-PSDB; AAV17288.

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for

PT diagnosis and therapy of cancer

XX Example 8; Page 100-101; 208pp; English.

XX This sequence is the light chain variable region of the antibody of
CC the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
CC with DNA encoding the antibody, are used to make the antibody or
CC conjugate. The conjugate is used in a medicament suitable for intravenous
CC administration. The conjugate can be used for cancer therapy, selectively
CC killing tumour cells. The antibody can be used for in vivo or in vitro
CC diagnosis of cancer.

XX Sequence 235 AA;

SQ Query Match 96.6%; Score 539; DB 18; Length 235;

Best Local Similarity 96.3%; Pred. No. 8.2e-31;

Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60

Db 23 DIELTQSPAIMASPGKVTITCSASSSVTYMHWFQKPGTSPKLIWYSTSNLASGVPAR 82

QY 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKR 107

Db 83 FSGSGGTSYSLTISRMEAEADAATYYCQQRSTYPLTFGAGTKLEIKR 129

RESULT 15

AAB82897

ID AAB82897 standard; Protein; 256 AA.

XX AAB82897;

XX 26-NOV-2001 (first entry)

DT Anti-p53 common mutant antigen single chain antibody ME1.

DE

XX Single chain antibody; ME1; mouse; p53; common mutant epitope;
KW tumour suppressor protein; therapy; cancer.

XX Mus musculus.

XX Key Location/Qualifiers

XX Region 1..131

XX Protein /label= Heavy_chain

XX Region 132..256

XX Region /label= Light_chain

XX Region 27..35

XX Region /label= CDR1

XX Region /note= "heavy chain complementarity determining

XX Region region 1"

XX Region 50..66

XX Region /label= CDR2

XX Region /note= "heavy chain complementarity determining

XX Region region 2"

XX Region 99..105

XX Region /label= CDR3

XX Region /note= "heavy chain complementarity determining

XX Region region 3"

XX Region 155..164

XX Region /label= CDR1

XX Region /note= "light chain complementarity determining

XX Region region 1"

XX Region 180..186

XX Region /label= CDR2

XX Region /note= "light chain complementarity determining

XX Region region 2"

XX Region 219..227

XX Region /label= CDR3

XX Region /note= "light chain complementarity determining

XX Region region 3"

XX WO200168801-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-IL00225.

XX 16-MAR-2000; 2000US-0526738.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Solomon B, Cohen G, Govorko D;

XX WPI; 2001-590047/66.

XX N-PSDB; AAH26790.

XX Novel single chain antibody molecule specifically recognizing common
PT mutant epitope in mutant p53 but not in wild-type p53, and
PT polynucleotides encoding antibodies, useful for preparing medicament
PT for treating cancer -
XX Claim 16; Fig 2A; 46pp; English.

XX The present sequence is that of a single chain antibody (scFv),
CC designated ME1, which specifically recognises the common mutant
CC epitope (see AAB82900) in mutant p53 protein but not in wild-type
CC p53. To obtain the scFv, mice were immunized with the mutant p53
CC epitope peptide. Gene segments encoding the antibody heavy and
CC light chain variable regions were amplified by PCR from the spleen
CC of a hyperimmunised mouse, and a library of the antibody genes was
CC obtained. When the genes isolated from the antibody gene library
CC were assembled in the scFv DNA, expressed as phage antibodies and
CC subjected to panning, scFv ME1 was isolated, which possessed a
CC significant affinity (0.1 uM) towards mutant p53. ME1 was
CC successfully expressed as a soluble antibody, separate from the
CC phage fusion. ME1, DNA encoding it (see AAH26790-91) and a vector
CC comprising the DNA, are used in claimed methods for treating a
CC patient suffering from a disease related to mutation of the p53

CC gene, especially cancer. scFv ME1 serves as a powerful auxiliary
CC agent capable of specifically enhancing the specificity and
CC effectiveness of the two major existing anti-cancer gene therapies.
CC Expression of the scFv ME1 molecules as an intrabody fused to the
CC F-box domain responsible for the targeting of the cell proteins to
CC the degradation cascade may be capable of significantly reducing
CC the level of mutant p53 in the cell, thereby broadening the range
CC of possible tumour targets for the original therapy. The
CC substitution of the original antibody by the scFv ME1 specific to
CC the mutant form of p53 may restrict the therapeutic effect to cancer
CC cells only, allowing a systemic application of this therapy. ME1
CC has high specificity, lacks the Fc portion which binds specifically
CC to the antigen, and has high permeability in the cells, and thus is
CC a suitable probe for immunodiagnostic clinical detection of mutant
CC p53 in tissues using conventional immunohistochemistry techniques.

xx
SQ Sequence 256 AA;

Query Match 96.1%; Score 536; DB 22; Length 256;
Best Local Similarity 95.4%; Pred. No. 1.4e-30;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGEKVTITCSASSSVSYMHWFQOKPGTSPKLIYSTSNLASGYPAR 60
Db |||||
132 DIETQSPAIMSASPGEKVTITCSASSSVNYMHWFQOKPGTSPKLIWISSTSNLASGYPAR 191

Qy 61 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
Db |||||
192 FSGSGGTSYSLTISRMEAEADAATYYCQQRSSYPFTFGSGTKLQIKRA 239

Search completed: December 23, 2002, 07:25:09
Job time : 50.9767 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 62.8081 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-7
Perfect score: 631
Sequence: 1 QVKLQQSGAELVGSASVKL.....AYYGDYEGYWGQGTTVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	117	21	AA197235
2	631	100.0	117	23	AAU74412
3	631	100.0	240	23	AAU74419
4	624	98.9	117	22	AAE13143
5	624	98.9	117	22	AA1982709
6	624	98.9	117	23	AAU74417
7	624	98.9	136	22	AA1982701
8	624	98.9	238	23	AAU74420
9	612	97.0	136	22	AAE13145
10	554.5	87.9	535	18	AAW28491

11	554.5	87.9	535	18	AAW28492	Human p53 protein
12	550.5	87.2	116	21	AA1970787	Murine anti-p53 mo
13	549.5	87.1	243	19	AAW60769	Single chain antib
14	532.5	84.4	112	20	AAW89173	Anti-p53 monoclon
15	532.5	84.4	118	18	AAW01586	Lead binding MAb 1
16	513.5	81.4	270	16	AA1975719	MFE-23 antibody.
17	513.5	81.4	556	22	AAU97935	scFv-rearranged ca
18	513.5	81.4	556	22	AAU80040	scFv-rearranged ca
19	507.5	80.4	124	15	AA1960566	Anti-carcinoembryo
20	507.5	80.4	249	19	AAW60770	Single chain antib
21	507.5	80.4	553	18	AAW11508	Single chain anti-
22	507.5	80.4	553	20	AAW73223	H22-anti-CEA antib
23	507.5	80.4	553	22	AA1985455	Bispecific single
24	507.5	80.4	553	22	AA1961960	Bispecific single
25	503.5	79.8	116	13	AA1924807	RSV19 VH. Mus mus
26	502.5	79.6	116	14	AA1942804	RSV19 heavy chain
27	502.5	79.6	124	15	AA1960565	Anti-carcinoembryo
28	499.5	79.2	116	14	AA1942802	RSV19 heavy chain
29	499.5	79.2	124	20	AA1939528	Murine COL1 VH cha
30	499.5	79.2	124	23	AAU76632	Murine Col-1(CEA a
31	498.5	79.0	120	18	AAW41387	Anti-CEA antibody
32	498.5	79.0	255	18	AAW41394	Chimeric anti-CEA
33	498.5	79.0	281	20	AAW82744	Fusion protein PIC
34	498.5	79.0	642	20	AAW82741	806.077 heavy chai
35	498.5	79.0	666	20	AAW82745	Fusion protein (80
36	494	78.3	119	12	AA194394	H3 region of MAB T
37	494	78.3	119	19	AAW48758	TA1 antibody VH ch
38	493	78.1	119	12	AA194395	Modified H3 region
39	487	77.2	140	12	AA191384	Variable gamma hea
40	486.5	77.1	258	23	AA1905962	Monoclonal antibod
41	486.5	77.1	258	23	AA1905990	Mouse monoclonal a
42	486.5	77.1	258	23	AA1905994	Mouse and human ch
43	486.5	77.1	287	23	AA1905982	Monoclonal antibod
44	484.5	76.8	120	16	AA1979889	Anti-EGFR antibody
45	481.5	76.3	135	21	AA197967	Amino acid sequenc

ALIGNMENTS

RESULT 1
AA197235
ID AA197235 standard; Protein; 117 AA.
XX
AC AA197235;
XX
DT 19-DEC-2000 (first entry)
XX
DE Variable heavy chain fragment of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determing region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Karposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;

XX WPI; 2000-505966/45.
DR N-PSDB; AAU53767.
XX Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX Claim 4; Page 50-51; 55pp; English.
XX New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX Sequence 117 AA;
SQ Query Match 100.0%; Score 631; DB 21; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
Db 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
QY 61 APKFQKATMTADSSNTAYLQLSLSLTSEDYAVYCNAYYGDYEGYWGQTTVTVSS 117
Db 61 APKFQKATMTADSSNTAYLQLSLSLTSEDYAVYCNAYYGDYEGYWGQTTVTVSS 117
RESULT 2
AAU74412
ID AAU74412 standard; peptide; 117 AA.
XX AAU74412;
AC AAU74412;
XX 26-MAR-2002 (first entry)
DT Antigen-binding protein heavy chain variable domain (VH) #1.
DE Antigen-binding protein; antibody heavy chain variable domain;
XX Cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX Mus sp.
OS WO200190192-A2.
XX 29-NOV-2001.
PD 24-MAY-2001; 2001WO-US16924.
XX 24-MAY-2000; 2000US-206749P.
PR (IMCL-) IMCLONE SYSTEMS INC.
XX Zhu Z;
PI WPI; 2002-106189/14.
XX N-PSDB; AAS20283.
XX

PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
XX two polypeptides and two second polypeptides
PS Claim 57; Page 57; 64pp; English.
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the FC region (e.g., CH2 and CH3 for an Igg molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX Sequence 117 AA;
SQ Query Match 100.0%; Score 631; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
Db 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
QY 61 APKFQKATMTADSSNTAYLQLSLSLTSEDYAVYCNAYYGDYEGYWGQTTVTVSS 117
Db 61 APKFQKATMTADSSNTAYLQLSLSLTSEDYAVYCNAYYGDYEGYWGQTTVTVSS 117
RESULT 3
AAU74419
ID AAU74419 standard; Protein; 240 AA.
XX AAU74419;
AC AAU74419;
XX 26-MAR-2002 (first entry)
DT Antigen-binding protein, single chain variable fragment version #1.
DE Antigen-binding protein; single chain variable fragment; scFv; antigen;
XX Cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX Mus sp.
OS Synthetic.
OS Key Location/Qualifiers
FH 1..117 /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"
FT 118..132 /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIGWIDPENGDSGY 60
|||||
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIGWIDPENGDSGY 60
|||||
QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTTVTVSS 117
|||||
Db 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTTVTVSS 117
|||||
RESULT 7
AAB82701
ID AAB82701 standard; Protein; 136 AA.
AC AAB82701;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..136
FT /label= Mature_protein
FT Region 45..54
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 59..85
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 118..125
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAH26413.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent .
XX
PS Disclosure; Fig 1; 42pp; English.
XX
CC The present sequence is that of the heavy chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an

CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 136 AA;
Query Match 98.9%; Score 624; DB 22; Length 136;
Best Local Similarity 99.1%; Pred. No. 3.3e-46;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSGY 60
|||||
Db 20 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSY 79
|||||
QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTTVTVSS 117
|||||
Db 80 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTTVTVSS 136
|||||
RESULT 8
AAU74420
ID AAU74420 standard; Protein; 238 AA.
XX
AC AAU74420;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #2.
XX
KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 61"
FT Region 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable fragment
FT protein. Encoded by AAS20285"
FT Region 133..238
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 61"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749p.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX

PI Zhu Z;
XX WPI; 2002-106189/14.
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 63; Page 62-63; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
CC invention.
XX
SQ Sequence 238 AA;
Query Match 98.9%; Score 624; DB 23; Length 238;
Best Local Similarity 99.1%; Pred. No. 5.9e-46;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPENGDSGY 60
Db 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPENGDSY 60
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117
Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117
RESULT 9
AAE13145
ID AAE13145 standard; Protein; 136 AA.
XX
AC AAE13145;
XX
DT 28-JAN-2002 (first entry)
XX Chimeric p1C11 heavy chain fragment.
DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytosstatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human; p1C11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader_peptide
FT Protein 20..136
FT /note= "Mature chimeric p1C11 heavy chain fragment"
FT Region 45..54

FT Region /label= CDR_H1
FT 69..85
FT /label= CDR_H2
FT Misc-difference 84
FT /note= "Residue 'O' is present at this location in the
FT sequence shown in fig-11 of the specification"
FT Misc-difference 101
FT /note= "Residue 'O' is present at this location in the
FT sequence shown in fig-11 of the specification"
FT 119..125
FT /label= CDR_H3
FT
XX WO200174296-A2.
PN 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10504.
PF 31-MAR-2000; 2000US-0540770.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafil S;
XX
XX WPI; 2001-662942/76.
DR N-PSDB; AAD21682.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow.
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1C11 heavy chain fragment which is used for the construction of chimeric
CC p1C11 IgG expression vector. Chimeric p1C11 heavy chain contains cloned
CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
CC domain (CH).
XX
SQ Sequence 136 AA;
Query Match 97.0%; Score 612; DB 22; Length 136;
Best Local Similarity 97.4%; Pred. No. 3.5e-45;
Matches 114; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPENGDSGY 60
Db 20 QVKLQSGAELVCGASVKLSCTTSGFNKIDFYMHVVKQRPEQGLEWIGWIDPENGDSY 79
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 117
Db 80 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGQGTVTVSS 136
RESULT 10
AAW28491
ID AAW28491 standard; Protein; 535 AA.
XX
AC AAW28491;
XX
DT 25-NOV-1997 (first entry)

XX DE Human p53 protein variant S-325 encoded by pEC176.
XX DE
XX KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX OS Chimeric - Homo sapiens.
OS Chimeric - Herpes simplex virus.
OS Synthetic.
XX XX
PN WO9704092-A1.
XX XX
PD 06-FEB-1997.
XX XX
PF 17-JUL-1996; 96WO-FR01111.
XX XX
PR 19-JUL-1995; 95FR-0008729.
XX XX
PA (RHON) RHONE POULENC RORER SA.
PI Bracco L, Conseiller E;
XX XX
DR WPI; 1997-132633/12.
DR N-PSDB; AAT86221.
XX XX
PT New p53 variants e.g. with oligomerisation domain replaced by
PT leucine zipper - useful for treating hyper-proliferative disorders,
PT esp. cancer and restenosis
XX XX
PS Claim 36; Pages 88-90; 133pp; French.
XX XX
CC Claimed variants of protein p53 have at least part of the
CC oligomerisation domain deleted and replaced by a leucine zipper
CC domain. The mutants preferably also have at least part of the p53
CC transactivation domain (amino acids 1-74) deleted and replaced by
CC the transactivating domain (TD) from herpes simplex virus viral
CC protein VP16 (amino acids 411-490) or by a protein domain able to
CC bind selectively to a transactivator, especially a single-chain
CC antibody variable domain (ScFv). The present sequence is that of
CC a specifically claimed p53 variant designated S-325 and comprising
CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a
CC leucine zipper domain at the C-terminal. The p53 variants are
CC more active and more stable tumour suppressors and apoptosis-inducing
CC agents than wild-type p53 and are active where the wild-type protein
CC is not, i.e. they are not inactivated by dominant negative or oncogenic
CC mutants, nor by other cellular proteins (because the leucine zipper
CC domain prevents formation of inactive mixed oligomers).
XX XX
SQ Sequence 535 AA;

Query Match 87.9%; Score 554.5; DB 18; Length 535;
Best Local Similarity 88.9%; Pred. No. 1.3e-39;
Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSGY 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 3 QVQLQESGAELVSGASVKLSCTASGNIKDYIMHWVKQRPEQGLEWIDPENGDT 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDTAVYYCNAYYGYEGYWGQTTVTVSS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 63 APKFQKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQTTVTVSS 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 11
AAW28492
ID AAW28492 standard; Protein; 535 AA.
XX
AC AAW28492;
XX
DT 25-NOV-1997 (first entry)
XX

DE DE Human p53 protein variant S-325H.
XX XX
KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX OS Chimeric - Homo sapiens.
OS Chimeric - Herpes simplex virus.
OS Synthetic.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 361 /note= "Arg residue at position 182 of wild-type
FT FT p53 has been mutated to His"
XX XX
PN WO9704092-A1.
XX XX
PD 06-FEB-1997.
XX XX
PF 17-JUL-1996; 96WO-FR01111.
XX XX
PR 19-JUL-1995; 95FR-0008729.
XX XX
PA (RHON) RHONE POULENC RORER SA.
XX XX
PI Bracco L, Conseiller E;
XX XX
DR WPI; 1997-132633/12.
XX XX
PT New p53 variants e.g. with oligomerisation domain replaced by
PT leucine zipper - useful for treating hyper-proliferative disorders,
PT esp. cancer and restenosis
XX XX
PS Claim 36; Page -; 133pp; French.
XX XX
CC Claimed variants of protein p53 have at least part of the
CC oligomerisation domain deleted and replaced by a leucine zipper
CC domain. The mutants preferably also have at least part of the p53
CC transactivation domain (amino acids 1-74) deleted and replaced by
CC the transactivating domain (TD) from herpes simplex virus viral
CC protein VP16 (amino acids 411-490) or by a protein domain able to
CC bind selectively to a transactivator, especially a single-chain
CC antibody variable domain (ScFv). The present sequence is that of
CC a specifically claimed p53 variant designated S-325H and comprising
CC a ScFv domain, amino acids 75-325 of human wild-type p53 (but with
CC Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
CC The p53 variants are more active and more stable tumour suppressors
CC and apoptosis-inducing agents than wild-type p53 and are active where
CC the wild-type protein is not, i.e. they are not inactivated by dominant
CC negative or oncogenic mutants, nor by other cellular proteins (because
CC the leucine zipper domain prevents formation of inactive mixed
CC oligomers).
CC (Note: this sequence does not appear in the specification and has
CC been produced by modifying the given sequence of variant V-325).
XX XX
SQ Sequence 535 AA;

Query Match 87.9%; Score 554.5; DB 18; Length 535;
Best Local Similarity 88.9%; Pred. No. 1.3e-39;
Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPEQGLEWIDPENGDSGY 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 3 QVQLQESGAELVSGASVKLSCTASGNIKDYIMHWVKQRPEQGLEWIDPENGDT 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 APKFQKATMTADSSNTAYLQLSSLTSEDTAVYYCNAYYGYEGYWGQTTVTVSS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 63 APKFQKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQTTVTVSS 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 12
AAW70787

ID XX AAY70787 standard; Protein; 116 AA.
AC XX AAY70787;
DT 31-JUL-2000 (first entry)
XX Murine anti-p53 monoclonal antibody PAb-421 heavy chain variable region.
DE
XX Murine; p53 protein; monoclonal antibody; PAb-421; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW heavy chain variable region; VH; complementarity determining region; CDR.
XX Mus sp.
OS
XX
FH Key Location/Qualifiers
FT Region 26..35
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region 50..66
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region 99..105
FT /label= CDR
FT /note= "Complementarity determining region"
XX WO200023082-A1.
PN
XX 27-APR-2000.
PD
XX 19-OCT-1999; 99WO-US24443.
PF
XX 19-OCT-1998; 98US-0104816.
PR
XX (YEDA) YEDA RES & DEV CO LTD.
PA
PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;
XX
XX WPI; 2000-339512/29.
DR
XX Treatment of systemic lupus erythematosus by down-regulating the
PT autoimmune response to the C-terminal DNA-binding domain of the p53
PT protein by an active compound comprising of antibodies to p53 or
PT fragments of p53 -
XX
PS Claim 78; Fig 9; 87pp; English.
XX
CC The patient discloses a method for the treatment of systemic lupus
CC erythematosus (SLE) by down-regulating the autoimmune response to the
CC C-terminal DNA-binding domain of p53 protein by an active compound.
CC The present sequence is a heavy chain variable region of monoclonal
CC antibody PAb-421 which is specific to the C-terminal DNA-binding domain
CC of murine p53 protein. PAb-421 antibody and peptides based on
CC complementarity determining regions of light and heavy chain variable
CC regions of the antibody, are examples of active compounds useful in the
CC diagnosis, prevention and treatment of SLE in humans.
XX
SQ Sequence 116 AA;
Query Match 87.2%; Score 550.5; DB 21; Length 116;
Best Local Similarity 88.9%; Pred. No. 5.6e-40;
Matches 104; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db 1 QVKLQESGAELVRSGASVKLSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDTY 60
QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYGYDYGWGQTTVTVSS 117
Db 61 APKFOGKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDWGQGTTVTVSS 116
RESULT 13

AAW60769
ID AAW60769 standard; Protein; 243 AA.
XX
AC AAW60769;
XX
DT 08-SEP-1998 (first entry)
XX
DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
XX
KW Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;
KW regulatory domain; p53 mutant; H273; W248; G281;
KW p53-dependent trans-activating activity; restoration;
KW tumour-suppressing activity; tumour cell; treatment;
KW hyper-proliferation; cancer; re-stenosis; ss.
XX
OS Mus sp.
XX
PN WO9818825-A1.
XX
PD 07-MAY-1998.
XX
PF 27-OCT-1997; 97WO-FR01921.
XX
PR 29-OCT-1996; 96FR-0013176.
XX
PA (RHON) RHONE-POULENC RORER SA.
XX
PI Debussche L, Bracco L;
XX
DR WPI; 1998-272140/24.
DR N-PSDB; AAV36236.
XX
PT Restoring p53-dependent trans-activating activity to cell containing
PT mutant p53 - by delivering single-chain antibody specific for the
PT mutant, particularly for treatment of tumours
XX
PS Claim 5; Page 31; 54pp; French.
XX
CC The present sequence represents a single chain antibody (ScFv) designated
CC 421. The antibody binds to an epitope present in the C-terminal region
CC of the p53 protein that includes oligomerisation and regulatory domains,
CC specifically between positions 320 and 393. ScFv 421 is directed against
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC introduced into cells containing a mutant p53 protein, p53-dependent
CC trans-activating activity is restored. ScFv 421 is specific for
CC p53-mutants that have lost tumour-suppressing activity and are present in
CC tumour cells. It is particularly used to treat hyper-proliferation
CC associated with these mutants (e.g. cancer and re-stenosis) but may also
CC be used in vitro for studying mechanisms of activity of p53 or its mutant
CC and to purify or detect p53.
XX
SQ Sequence 243 AA;
Query Match 87.1%; Score 549.5; DB 19; Length 243;
Best Local Similarity 88.9%; Pred. No. 1.5e-39;
Matches 104; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
Db 1 QVKLQSGAELVRSGASVKLSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDTY 60
QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYGYDYGWGQTTVTVSS 117
Db 61 APKFOGKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDWGQGTTVTVSS 116
RESULT 14
AAW89173
ID AAW89173 standard; peptide; 112 AA.
XX
AC AAW89173;
XX
DT 25-MAR-1999 (first entry)

XX DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.

XX KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;

XX KW immune response; tumour associated antigen; metastatic cancer.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO9856416-A1.

XX PD 17-DEC-1998.

XX PF 09-JUN-1998; 98WO-IL00266.

XX PR 09-JUN-1997; 97IL-0121041.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;

XX PI Wolkowicz R;

XX DR WPI; 1999-070296/06.

XX PT Use of a monoclonal antibody to a tumour-associated antigen - to

XX PT induce anti-tumour immunity or elicit an increased immune response

XX PT to the antigen

XX PS Example 3; Fig 3; 47pp; English.

XX CC The present invention describes the use of an immunogen (A) to induce

XX CC anti-tumour immunity; to elicit an increased immune response to tumour

XX CC associated antigen (TAA) and/or to induce an immune response to mutant

XX CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody

XX CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR

XX CC (complementarity determining region) on the heavy or light chain of MAB

XX CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the

XX CC variable (V) region of MAB, in a gene delivery vehicle. The present

XX CC sequence represents the variable heavy chain sequence from anti-p53 MAB

XX CC 421. Also described is a method for generating sequence-specific,

XX CC anti-DNA antibodies (Ab) by immunising a mammal with a MAB directed to a

XX CC domain containing a DNA-binding site of a DNA-binding protein. (A) is

XX CC used to treat a wide variety of primary and metastatic cancers,

XX CC particularly those where p53 is involved. Ab are used for diagnosis (e.g

XX CC to determine critical sequences in animal or plant breeding); to

XX CC identify bacteria and other parasites; to determine parentage; in

XX CC forensic science; to isolate specific genes for DNA vaccination; in gene

XX CC sequencing and cloning; also possibly for activation of selected

XX CC therapeutic genes in plants, animals and humans. (A) induce an effective

XX CC anti-tumour response without causing harm to the patient. The method

XX CC uses (A) to generate anti-TAA by exploiting the anti-idiotype network.

XX SQ Sequence 112 AA;

Query Match 84.4%; Score 532.5; DB 20; Length 112;

Best Local Similarity 88.5%; Pred. No. 1.9e-38;

Matches 100; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 LQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGYAPK 63

Db 1 LQESGAELVRSGASVKLSCTASGFNKKDYIMHWVKORPEQGLEWIGWIDPENGDTYAPK 60

QY 64 FQKATMTADSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTVS 116

Db 61 FQKATMTADTSSNTAYLQLSLASEDTAVYYCN-FYGDALDYWGQTTVTVS 112

RESULT 15

AAW01586

ID AAW01586 standard; Protein; 118 AA.

XX AC

XX AAW01586;

DT 22-AUG-1997 (first entry)

XX Lead binding MAB 14G11 heavy chain variable region.

DE Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;

XX KW pharmaceutical; health care; skin treatment; pesticide; herbicide;

XX KW heavy metal.

XX OS Mus musculus.

XX PN WO9639518-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US09258.

XX PR 10-OCT-1995; 95US-0541373.

XX PR 05-JUN-1995; 95US-0462798.

XX PA (BION-) BIONEBRASKA INC.

XX PI Lopez O, Murray PJ, Wylie DE;

XX DR WPI; 1997-043140/04.

XX DR N-PSDB; AAT58260.

XX PT DNA encoding heavy metal binding polypeptide sequences - used for

XX PT detecting, removing, adding or neutralising heavy metals, such as

XX PT lead cations

XX PS Claim 12; Page 75; 125pp; English.

XX CC The present sequence represents the heavy chain variable region for

XX CC monoclonal antibody (Mab) 14G11, which immunoreacts with a lead cation.

XX CC The sequence was derived from RNA isolated from mouse hybridoma cells.

XX CC The protein can be used for binding heavy metals, such as lead cations.

XX CC It can be used for detecting, removing, adding or neutralising the

XX CC heavy metals in biological and inanimate systems. It can be used in

XX CC e.g. aqueous liquid systems, in biological or environmental systems or

XX CC in such compositions as perfumes, cosmetics, pesticides, herbicides,

XX CC care products, skin treatment products, semi-conductor and integrated

XX CC solvents used in the production of electronic components.

XX CC circuit components and production materials for electronic components.

XX CC The products can provide for applications involving minute amounts of

XX CC specific heavy metals.

XX SQ Sequence 118 AA;

Query Match 84.4%; Score 532.5; DB 18; Length 118;

Best Local Similarity 85.6%; Pred. NO. 2e-38;

Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVKLQQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60

Db 1 EVQLQQSGAELVRSGASVKLSCTASGFNKKDYIMHWVKORPEQGLEWIGWIDPENGDTY 60

QY 61 APKFQKATMTADSSNTAYLQLSLTSEDYAVYYCNAY-YGDYEGYWGQTTVTVS 117

Db 61 DPKFQKATMTADTSSNIAYLQLSLTSEDYAVYYCNFYCYDDAMDYWGQTSVTVS 118

Search completed: December 23, 2002, 07:25:08

Job time : 64.8081 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 1.80233 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	2	US-08-116-778E-9
2	48	100.0	10	2	US-08-438-562-9
3	48	100.0	10	2	US-08-483-528B-97
4	48	100.0	10	3	US-08-836-561-49
5	48	100.0	10	4	US-09-393-385B-108
6	48	100.0	97	4	US-09-280-028-4
7	48	100.0	100	2	US-08-308-494A-19
8	48	100.0	105	3	US-08-434-000A-12
9	48	100.0	105	4	US-09-312-157-12
10	48	100.0	110	3	US-08-836-561-33
11	48	100.0	129	2	US-08-116-778E-2
12	48	100.0	129	2	US-08-438-562-2
13	48	100.0	129	2	US-08-483-528B-92
14	48	100.0	130	4	US-09-393-385B-111
15	48	100.0	130	4	US-09-393-385B-113
16	48	100.0	133	2	US-08-116-778E-37
17	48	100.0	133	2	US-08-438-562-37
18	48	100.0	133	2	US-08-483-528B-101
19	48	100.0	222	2	US-08-190-199A-67
20	48	100.0	235	2	US-08-190-199A-61
21	48	100.0	270	2	US-08-652-507-2
22	48	100.0	553	2	US-08-661-052-16
23	48	100.0	553	4	US-09-188-082-16
24	48	100.0	553	4	US-09-364-088-16
25	48	100.0	553	4	US-09-102-716-16
26	47	97.9	106	1	US-07-634-278-1
27	47	97.9	106	1	US-07-634-278-7

28	47	97.9	106	1	US-07-634-278-8	Sequence 8, Appli
29	47	97.9	106	1	US-07-634-278-16	Sequence 16, Appl
30	47	97.9	106	1	US-08-477-728-1	Sequence 1, Appli
31	47	97.9	106	1	US-08-477-728-7	Sequence 7, Appli
32	47	97.9	106	1	US-08-477-728-8	Sequence 8, Appli
33	47	97.9	106	1	US-08-477-728-16	Sequence 16, Appl
34	47	97.9	106	1	US-08-474-040-1	Sequence 1, Appli
35	47	97.9	106	1	US-08-474-040-7	Sequence 7, Appli
36	47	97.9	106	1	US-08-474-040-8	Sequence 8, Appli
37	47	97.9	106	1	US-08-474-040-16	Sequence 16, Appl
38	47	97.9	106	1	US-08-487-200-1	Sequence 1, Appli
39	47	97.9	106	1	US-08-487-200-7	Sequence 7, Appli
40	47	97.9	106	1	US-08-487-200-8	Sequence 8, Appli
41	47	97.9	106	1	US-08-487-200-16	Sequence 16, Appl
42	47	97.9	106	1	US-08-488-113B-163	Sequence 163, App
43	47	97.9	106	1	US-08-488-113B-165	Sequence 165, App
44	47	97.9	106	1	US-08-477-484B-163	Sequence 163, App
45	47	97.9	106	1	US-08-477-484B-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-08-116-778E-9
; Sequence 9, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-116-778E-9

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASSSVSYMH 10
|||||

Db 1 SASSSVSYMH 10

RESULT 2

US-08-438-562-9
; Sequence 9, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-438-562-9

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches :10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 1 SASSSVSYMH 10

RESULT 3

US-08-483-528B-97
; Sequence 97, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-528B-97

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches :10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 1 SASSSVSYMH 10

RESULT 4

US-08-836-561-49
; Sequence 49, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, AKIKO
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, AKIHIRO
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736

; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-561-49

Query Match 100.0%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
| | | | | | | | | |
Db 1 SASSSVSVMH 10

RESULT 5

US-09-393-385B-108
; Sequence 108, Application US/09393385B
; Patent No. 6423511

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96

; CLASSIFICATION:

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 108:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-393-385B-108

Query Match 100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
| | | | | | | | | |
Db 1 SASSSVSVMH 10

RESULT 6

US-09-280-028-4
; Sequence 4, Application US/092800028
; Patent No. 6241961

; GENERAL INFORMATION:

; APPLICANT: BENES, IVAN FRIEDRICH
; APPLICANT: BOSSLET, KLAUS
; TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
; TITLE OF INVENTION: METHOD FOR THEIR PREPARATION
; FILE REFERENCE: BENES
; CURRENT APPLICATION NUMBER: US/09/280,028
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 199 11 329.7
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: 198 13 687.0
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

; LENGTH: 97

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-280-028-4

Query Match 100.0%; Score 48; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 0.038;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
| | | | | | | | | |
Db 16 SASSSVSVMH 25

RESULT 7

US-08-308-494A-19
; Sequence 19, Application US/08308494A
; Patent No. 5959083

; GENERAL INFORMATION:

; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/308,494A

; FILING DATE: 21-SEP-1994

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/891,739

; FILING DATE: 01-JUN-1992

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P4118120.4

; FILING DATE: 03-JUN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Kulik, David J.

; REGISTRATION NUMBER: 36,576

; REFERENCE/DOCKET NUMBER: 05552-1186-02000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-019

Query Match 100.0%; Score 48; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 21 SASSSVSYMH 30

RESULT 8

US-08-434-000A-12
Sequence 12, Application US/08434000A
Patent No. 6046037

GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 1
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLGY: DESCRIPTION: Guy's 13 Kappa

US-08-434-000A-12

Query Match 100.0%; Score 48; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 9

US-09-312-157-12
Sequence 12, Application US/09312157
Patent No. 6303341

GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351

SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12: Guy's 13 Kappa

US-09-312-157-12

Query Match 100.0%; Score 48; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 10

US-08-836-561-33
Sequence 33, Application US/08836561
Patent No. 6018032

GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
APPLICANT: FURUYA, Akiko
APPLICANT: NAKAMURA, Kazuyasu

APPLICANT: IIDA, Akihiro
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, NO. 6018032uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-561-33

Query Match 100.0%; Score 48; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
Db 27 SASSSVSYMH 36

RESULT 11
US-08-116-778E-2
Sequence 2, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-116-778E-2

Query Match 100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
Db 46 SASSSVSYMH 55

RESULT 12
US-08-438-562-2
Sequence 2, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2

Query Match 100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches: 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 46 SASSSSVSYMH 55

RESULT 13
US-08-483-528B-92
; Sequence 92, Application US/08483528B

Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-483-528B-92

Query Match 100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches: 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
Db 46 SASSSSVSYMH 55

RESULT 14

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US-09-393-385B-111
; Sequence 111, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-393-385B-111

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Query Match      100.0%; Score 48; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SASSSVSYMH 10
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Db 46 SASSSVSYMH 55

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RESULT 15

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US-09-393-385B-113
; Sequence 113, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-393-385B-113

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Query Match      100.0%; Score 48; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SASSSVSYMH 10
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Db 46 SASSSVSYMH 55

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Search completed: December 23, 2002, 07:33:14
Job time : 2.80233 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 1.26163 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
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1	31	100.0	7	2	US-08-116-778E-10		Sequence 10, Appl
2	31	100.0	7	2	US-08-438-562-10		Sequence 10, Appl
3	31	100.0	7	2	US-08-483-528B-98		Sequence 98, Appl
4	31	100.0	7	4	US-09-171-945-27		Sequence 27, Appl
5	31	100.0	7	4	US-09-393-385B-109		Sequence 109, App
6	31	100.0	100	2	US-08-308-494A-15		Sequence 15, Appl
7	31	100.0	105	3	US-08-434-000A-12		Sequence 12, Appl
8	31	100.0	105	4	US-09-312-157-12		Sequence 12, Appl
9	31	100.0	107	4	US-09-171-945-50		Sequence 50, Appl
10	31	100.0	107	4	US-09-171-945-61		Sequence 61, Appl
11	31	100.0	107	4	US-09-171-945-65		Sequence 65, Appl
12	31	100.0	107	4	US-09-171-945-71		Sequence 71, Appl
13	31	100.0	108	3	US-08-483-749A-8		Sequence 8, Appli
14	31	100.0	108	4	US-09-171-945-9		Sequence 9, Appli
15	31	100.0	129	2	US-08-116-778E-2		Sequence 2, Appli
16	31	100.0	129	2	US-08-438-562-2		Sequence 2, Appli
17	31	100.0	129	2	US-08-483-528B-92		Sequence 92, Appl
18	31	100.0	130	4	US-09-393-385B-111		Sequence 111, App
19	31	100.0	130	4	US-09-393-385B-113		Sequence 113, App
20	31	100.0	133	2	US-08-116-778E-37		Sequence 37, Appl
21	31	100.0	133	2	US-08-438-562-37		Sequence 37, Appl
22	31	100.0	133	2	US-08-483-528B-101		Sequence 101, App
23	31	100.0	213	3	US-08-630-820-6		Sequence 6, Appli
24	31	100.0	215	6	5455030-3		Patent No. 5455030
25	31	100.0	225	6	5455030-5		Patent No. 5455030
26	31	100.0	235	4	US-09-171-945-17		Sequence 17, Appl
27	31	100.0	235	4	US-09-171-945-52		Sequence 52, Appl

28	31	100.0	235	4	US-09-171-945-97	Sequence 97, Appl
29	31	100.0	235	4	US-09-171-945-99	Sequence 99, Appl
30	31	100.0	236	6	5455030-7	Patent No. 5455030
31	31	100.0	244	1	US-08-230-843-2	Sequence 2, Appli
32	31	100.0	244	2	US-08-636-936-2	Sequence 2, Appli
33	31	100.0	247	6	5455030-9	Patent No. 5455030
34	31	100.0	248	6	5455030-11	Patent No. 5455030
35	31	100.0	270	2	US-08-652-507-2	Sequence 2, Appli
36	31	100.0	281	4	US-09-423-439-44	Sequence 44, Appl
37	31	100.0	553	2	US-08-661-052-16	Sequence 16, Appl
38	31	100.0	553	4	US-09-188-082-16	Sequence 16, Appl
39	31	100.0	553	4	US-09-364-088-16	Sequence 16, Appl
40	31	100.0	553	4	US-09-102-716-16	Sequence 16, Appl
41	31	100.0	666	4	US-09-423-439-51	Sequence 51, Appl
42	28	90.3	7	3	US-08-783-853A-13	Sequence 13, Appl
43	28	90.3	7	4	US-09-280-028-14	Sequence 14, Appl
44	28	90.3	7	4	US-09-344-050-13	Sequence 13, Appl
45	28	90.3	20	1	US-07-678-974D-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-116-778E-10
; Sequence 10, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-778E-10

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
|||||||

Db 1 STSNLAS 7

RESULT 2

US-08-438-562-10
; Sequence 10, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-438-562-10

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 3
US-08-483-528B-98
; Sequence 98, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

US-08-438-562-10
; Sequence 10, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-528B-98

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 4
US-09-171-945-27
; Sequence 27, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-27
; Sequence 27, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-27
; Sequence 27, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized

QY 1 STSNLAS 7

Db 1 STSNLAS 7

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-393-385B-109
; Sequence 109, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-393-385B-109

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 1 STSNLAS 7

RESULT 6
US-08-308-494A-15
; Sequence 15, Application US/08308494A
; Patent No. 5959083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-15

Query Match 100.0%; Score 31; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 46 STSNLAS 52

RESULT 7
US-08-434-000A-12
; Sequence 12, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
```

REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: DESCRIPTION: Guy's 13 Kappa
US-08-434-000A 12

Query Match 100.0%; Score 31; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 8
US-09-312-157-12
Sequence 12, Application US/09312157
Patent No. 6303341
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351
SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: Guy's 13 Kappa
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-312-157-12

Query Match 100.0%; Score 31; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 9
US-09-171-945-50
Sequence 50, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-50

Query Match 100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 10
US-09-171-945-61
Sequence 61, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence


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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-61

Query Match          100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 49 STSNLAS 55

RESULT 11
US-09-171-945-65
; Sequence 65, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-65

Query Match          100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
   |||||
Db 49 STSNLAS 55

RESULT 12
US-09-171-945-71
; Sequence 71, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-71

Query Match          100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 49 STSNLAS 55

RESULT 13
US-08-483-749A-8
; Sequence 8, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-8

Query Match          100.0%; Score 31; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 51 STSNLAS 57

RESULT 14
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
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;; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
;; FILE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
;; CURRENT APPLICATION NUMBER: US/09/171,945
;; CURRENT FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: GB9703103.3
;; PRIOR FILING DATE: 1997-02-14
;; PRIOR APPLICATION NUMBER: GB9609405.7
;; PRIOR FILING DATE: 1996-05-04
;; PRIOR APPLICATION NUMBER: PCT/GB97/01165
;; PRIOR FILING DATE: 1997-04-29
;; NUMBER OF SEQ ID NOS: 131
;; SOFTWARE: Patent Ver. 2.1
;; SEQ ID NO 9
;; LENGTH: 108
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match 100.0%; Score 31; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 15

US-08-116-778E-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

;; NAME/KEY: sig_peptide
;; LOCATION: -22..-1
;; IDENTIFICATION METHOD: BY SIMILARITY
;; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
;; IDENTIFICATION METHOD: CONSENSUS
;; FEATURE:
;; NAME/KEY: domain
;; LOCATION: 24..33
;; IDENTIFICATION METHOD: BY SIMILARITY
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;; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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;; NAME/KEY: domain
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;; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
;; IDENTIFICATION METHOD: CONSENSUS
;; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-116-778E-2

Query Match 100.0%; Score 31; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 71 STSNLAS 77

Search completed: December 23, 2002, 07:33:14
Job time : 1.26163 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 3.75775 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	AAW41383	CDR2 of light chai
2	31	100.0	7	AAW73170	CDR2 of light chai
3	31	100.0	7	AAZ28391	Peptide fragment f
4	31	100.0	7	AAZ97233	Complementary dete
5	31	100.0	7	AAZ10005	H. pylori 26 kDa p
6	31	100.0	7	AAE13141	Humanised antibody
7	31	100.0	7	AAB82707	VEGF antagonist an
8	31	100.0	7	AAB81968	Ganglioside GD2 sp
9	31	100.0	7	AAB83164	Mouse ganglioside
10	31	100.0	7	AAG63992	Complementarity de

11	31	100.0	7	23	AAU81254	Murine trkC antibo
12	31	100.0	7	23	AAU74410	Light chain comple
13	31	100.0	8	23	AAG80315	Anti-human TNF-alp
14	31	100.0	92	20	AAW89175	Anti-p53 monoclonal
15	31	100.0	93	23	ABP02151	Human ORFX protein
16	31	100.0	100	11	AAU07319	VK domain of antib
17	31	100.0	100	17	AAW14487	Monoclonal antibod
18	31	100.0	100	17	AAU99876	Monoclonal antibod
19	31	100.0	102	22	AAB62264	Light chain constr
20	31	100.0	105	17	AAW03182	Guy's 13 anti-Stre
21	31	100.0	106	22	AAE13144	Humanised antibody
22	31	100.0	106	23	AAU74418	Antigen-binding pr
23	31	100.0	107	18	AAW41397	Anti-CEA antibody
24	31	100.0	107	18	AAW41400	Humanised antibody
25	31	100.0	107	18	AAW41401	Humanised antibody
26	31	100.0	107	18	AAW41390	Anti-CEA antibody
27	31	100.0	107	22	AAB83159	Mouse ganglioside
28	31	100.0	107	22	AAB83167	Ganglioside GM2 an
29	31	100.0	107	22	AAG63987	Amino acid sequenc
30	31	100.0	108	13	AAU21294	Murine VL kappa gr
31	31	100.0	108	13	AAU21290	Murine VL kappa gr
32	31	100.0	108	16	AAU79884	Anti-EGFR antibody
33	31	100.0	108	18	AAW41388	Anti-CEA antibody
34	31	100.0	108	21	AAU97236	Variable light cha
35	31	100.0	108	21	AAB10021	H. pylori 26 kDa p
36	31	100.0	108	21	AAU90815	33F8 hybridoma VL
37	31	100.0	108	21	AAU53591	Light chain from a
38	31	100.0	108	21	AAU59306	DC8 light chain va
39	31	100.0	108	22	AAB82710	VEGF antagonist an
40	31	100.0	108	23	AAU74413	Antigen-binding pr
41	31	100.0	108	23	AAG80318	Anti-human TNF-alp
42	31	100.0	109	22	AAB81971	Ganglioside GD2 sp
43	31	100.0	109	22	AAB81974	Ganglioside GD2 sp
44	31	100.0	109	23	AAU81278	Murine trkC antibo
45	31	100.0	110	13	AAU21287	Murine VL kappa gr

ALIGNMENTS

RESULT 1

AAW41383

ID AAW41383 standard; peptide; 7 AA.

AC AAW41383;

DT 02-JUN-1998 (first entry)

DE CDR2 of light chain of anti-CEA antibody.

KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
cancer diagnosis; complementarity determining region; light chain.

OS Synthetic.

PN WO9742329-A1.

PD 13-NOV-1997.

PF 29-APR-1997; 97WO-GB01165.

PR 14-FEB-1997; 97GB-0003103.

PR 04-MAY-1996; 96GB-0009405.

XX (ZENE) ZENECA LTD.

PI Copley CG, Edge MD, Emery SC;

DR WPI; 1997-558987/51.

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
diagnosis and therapy of cancer

PS Claim 1; Page 196; 208pp; English.

XX This sequence represents a complementarity determining region (CDR) of

CC the light chain of the antibody of the invention. The antibody is an

CC anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or

CC transgenic organisms transformed with DNA encoding the antibody, are used

CC to make the antibody or conjugate. The conjugate is used in a medicament

CC suitable for intravenous administration. The conjugate can be used for

CC cancer therapy, selectively killing tumour cells. The antibody can be

CC used for in vivo or in vitro diagnosis of cancer.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 2

AAW73170

ID AAW73170 standard; peptide; 7 AA.

XX

AC AAW73170;

XX

DT 22-JAN-1999 (first entry)

XX

DE CDR2 of light chain of ganglioside GM2 targeting antibody.

XX

KW Ganglioside GM2; antibody; complementarity determining region; cancer;

XX anti-tumour agent.

OS Homo sapiens.

XX

PN JP10257893-A.

XX

PD 29-SEP-1998.

XX

PF 19-MAR-1997; 97JP-0066981.

XX

PR 19-MAR-1997; 97JP-0066981.

XX

PA (KYOW) KYOWA HAKKO KOGYO KK.

XX

DR WPI; 1998-575904/49.

XX

PT A human type complementarity determining region transplanted

PT antibody against ganglioside GM2 - useful as an anti-tumour agent

PT and as a diagnostic for related cancers

XX

PS Claim 1; Page 29; 66pp; Japanese.

XX

CC This sequence represents a complementarity determining region (CDR) from

CC the heavy chain of the antibody of the invention. The antibody of the

CC invention is a human CDR transplanted antibody that reacts specifically

CC with ganglioside GM2. DNA encoding the antibody, and vectors and

CC transformants containing it, can be used for the recombinant production

CC of the antibody. The antibody itself can be used as an anti-tumour agent

CC or as a diagnostic tool for related cancers. The antibody has antitumour

CC activity against ganglioside GM2 positive cells.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 3

AAW73170

ID AAY28391 standard; Protein; 7 AA.

XX

AC AAY28391;

XX

DT 04-NOV-1999 (first entry)

XX

DE Peptide fragment from the human anti-GM2 light chain in REI.

XX

KW antibody; REI; complementarity determining region; CDR;

XX chimeric; light chain; heavy chain.

OS Homo sapiens.

XX

PN US5939532-A.

XX

PD 17-AUG-1999.

XX

PF 07-JUN-1995; 95US-0483528.

XX

PR 07-JUN-1995; 95US-0483528.

PR 07-SEP-1993; 93US-0116778.

XX

PA (KYOW) KYOWA HAKKO KOGYO KK.

XX

PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;

PI Shitara K;

XX

DR WPI; 1999-468416/39.

XX

PT Chimeric human antibody expression vectors

XX

PS Example 2; Column 157; 188pp; English.

XX

CC The sequences AAY28390 to AAY28392 replace the CDR regions of the NEWM

CC DNA and they produce AAY28394, the hKM796L human anti-GM2 antibody light

CC chain.

CC Chimeric human antibodies of the invention are useful in the treatment

CC of cancer, especially that which is of neural ectodermal origin.

CC In contrast to prior art constructs based on mouse monoclonal

CC antibodies, the chimeric human antibodies do not cause anti-mouse

CC immunoglobulin production.

CC The chimeric human antibodies have a prolonged half-life and a reduced

CC frequency of adverse effects when compared to mouse monoclonal

CC antibodies.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 4

AAW7233

ID AAY97233 standard; Protein; 7 AA.

XX

AC AAY97233;

XX

DT 19-DEC-2000 (first entry)

XX

DE Complementary determining region (CDRL2) of anti-SI(KDR) antibody.

XX

KW Immunoglobulin; antibody; complementary determining region; CDR;

KW VEGF; vascular endothelial growth factor; KDR;

KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;
XX
DR WPI; 2000-505966/45.
DR N-PSDB; AAA53765.
XX
XX Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 3; Page 50; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 1 STSNLAS 7

RESULT 5
AAB10005
ID AAB10005 standard; Protein; 7 AA.
XX
AC AAB10005;
XX
DT 01-NOV-2000 (first entry)
XX
DE H. pylori 26 kDa protein-binding antibody light chain CDR2 peptide.
XX
KW Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; light chain; complementarity determining region;
KW CDR.
XX Unidentified.
OS
XX

PN WO200026671-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-EP08212.
XX
PR 29-OCT-1998; 98EP-0120517.
PR 06-NOV-1998; 98EP-0120687.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
PI Ringeis A;
XX
DR WPI; 2000-365747/31.
DR N-PSDB; AAA40161.
XX
PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT pylori, comprises reacting a faecal sample with two binding reagents for
PT antigens that survive intestinal passage -
XX
PS Claim 24; Page 21; 84pp; German.
XX
CC This invention describes a novel method for the detection of a mammalian
CC infection by an acid-resistant microorganism (A) by treating a faecal
CC sample with at least two different monoclonal antibodies (MAB) (or their
CC fragments or derivatives) or aptamers (collectively (I)) and detecting
CC formation of a complex (C) between (I) and the corresponding antigen of
CC (A). The first and second (I) bind to epitopes of different antigens
CC (Ag). These epitopes are present, after passage through the intestines,
CC in at least some mammals, and have either: (i) their native structure;
CC or (ii) a structure against which an antibody is produced by an animal
CC infected or immunized with (A), or its extract, lysate, derived protein
CC or fragment, or with a synthetic peptide. Practically all mammals display
CC at least one of the specified epitopes. The method is used to detect
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
CC therapeutically. The method is direct and non-invasive, and provides an
CC inexpensive and easily standardizable diagnosis, despite possible
CC degradation of antigens during passage through the intestines. This
CC sequence represents a fragment of a H. pylori 26 kDa protein-binding
CC antibody light chain complementarity determining region CDR2 which is
CC used to illustrate the method of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 1 STSNLAS 7

RESULT 6
AAE13141
ID AAE13141 standard; peptide; 7 AA.
XX
AC AAE13141;
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody murine light chain hypervariable region (VL) CDR2.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain hypervariable region; VL; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
XX
OS Mus sp.
XX

PN WO200174296-A2.
XX 11-OCT-2001;
PD 30-MAR-2001; 2001WO-US10504.
XX 31-MAR-2000; 2000US-0540770.
PR (IMCL-) IMCLONE SYSTEMS INC.
XX (CORR) CORNELL RES FOUND INC.
PI Witte L, Rafii S;
XX WPI; 2001-662942/76.
DR N-PSDB; AAD21667.
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX Claim 8; Page 15; 68pp; English.
PS The invention relates to a method for inhibiting the growth of non-solid
XX tumor cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody murine light chain hypervariable region (VL) CDR-2 used in the
CC exemplification of the invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db |||||
1 STSNLAS 7
RESULT 7
AAB82707
ID AAB82707 standard; Peptide; 7 AA.
XX AAB82707;
XX 15-OCT-2001 (first entry)
DT VEGF antagonist antibody IMC-1C11 VL CDR-2.
XX
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
KW complementarity determining region.
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200154723-A1.
XX 02-AUG-2001.
PD
XX

PF 29-JAN-2001; 2001WO-US02839.
XX 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX Kerbel R;
XX WPI; 2001-514531/56.
DR Treating or controlling an angiogenic dependent condition (e.g. a
XX neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX Disclosure; Page 37; 42pp; English.
PS The present sequence is that of complementarity determining region
XX 2 of the light chain variable region (see also AAB82702) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db |||||
1 STSNLAS 7
RESULT 8
AAB81968
ID AAB81968 standard; Peptide; 7 AA.
XX AAB81968;
XX 03-JUL-2001 (first entry)
DT Ganglioside GD2 specific antibody related peptide SEQ ID NO: 7.
XX Ganglioside; GD2; complementation determining region; CDR; antibody;
KW mouse; cancer.
XX Mus musculus.
OS WO200123573-A1.
XX 05-APR-2001.
PD 29-SEP-2000; 2000WO-JP06773.
XX 30-SEP-1999; 99JP-0278290.
PR

XX (KYOW) KYOWA HAKKO KOGYO KK.
PA Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266163/27.
DR
XX Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumours, has low antigenicity, little side effects but potent
PT activity in cancer -
XX
PS Claim 6; Page 100; 123pp; Japanese.
XX
CC The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumours,
CC particularly cancer diagnosis. The present sequence is a peptide
CC used in the exemplification of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db | | | | | | |
1 STSNLAS 7

RESULT 9
AAB83164
ID AAB83164 standard; peptide; 7 AA.
XX
AC AAB83164;
XX
DT 02-JUL-2001 (first entry)
XX
DE Mouse ganglioside GM2 antibody light chain variable region CDR2.
XX
KW Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer;
KW complementarity determining region; CDR.
XX
OS Mus sp.
XX
PN WO200123431-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP06775.
XX
PR 30-SEP-1999; 99JP-0278292.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Nakamura K, Niwa R;
XX
WPI; 2001-266142/27.
XX
PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
PT radioisotopes or proteins for treatment and diagnosis of cancer -
XX
PS Claim 4; Page 72; 80pp; Japanese.
XX
CC The present invention relates to derivatives of an antibody against
CC ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope,
CC protein or small drug in the treatment and diagnosis of cancer.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db | | | | | | |
1 STSNLAS 7

RESULT 10
AAG63992
ID AAG63992 standard; peptide; 7 AA.
XX
AC AAG63992;
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region of light chain of antibody 2C4.
XX
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX
PN WO200166126-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07193.
XX
PR 07-MAR-2000; 2000US-0187595.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX
WPI; 2001-570749/64.
XX
PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal -
XX
PS Claim 10; Page 34; 35pp; English.
XX
CC AAG63991-93 represent the complementarity determining regions (CDRs)
CC of the light chain variable region of murine monoclonal antibody 2C4.
CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The
CC antibody is useful for treating or preventing allergic rhinitis,
CC allergies, asthma, anemia, eczema or diseases such as lymphoma,
CC leukemia or systemic mastocytosis in a mammal. It is also useful for
CC detecting the presence of a cell, especially eosinophil in a sample,
CC by detecting binding of the antibody to SAF-2. The antibody can be
CC coupled to toxins, antiproliferative drugs or radionuclides to
CC kill cells in areas of excessive SAF-2 expression.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db | | | | | | |
1 STSNLAS 7

RESULT 11
AAU81254
ID AAU81254 standard; Peptide; 7 AA.

XX AAU81254;
AC
XX
DT 09-APR-2002 (first entry)
XX
DE Murine trkC antibody light chain CDR2 of variable region #2.
XX
KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;
KW basopaenia; lymphopaenia; monocytopenia; neutropenia; cancer; ulcer;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
KW cellular degeneration; gene therapy.
OS Mus sp.
XX
XX WO200198361-A2.
PN
XX
PD 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US20153.
PF
XX 22-JUN-2000; 2000US-213141P.
PR 05-OCT-2000; 2000US-238319P.
XX
PA (GETH) GENENTECH INC.
XX
PI Devaux B; Hongo JS, Presta LG, Shelton DL;
XX
XX WPI; 2002-130790/17.
DR
XX Novel anti-trkC agonist monoclonal antibody useful for treating
PT neurodegenerative disease, shows no significant cross-reactivity with
PT trkA/trkB, and recognizes epitope in domain 5 of trkC -
XX
PS Claim 13; Fig 11; 121pp; English.
XX
XX The invention relates to an anti-trkC agonist monoclonal antibody which
CC shows no significant cross-reactivity with trkA or trkB, and recognizes
CC an epitope in domain 5 of trkC. The antibodies of the invention are
CC effective in the treatment of cisplatin- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
CC cells such as leukopaenia including eosinopaenia, basopaenia,
CC lymphopaenia, monocytopenia, neutropenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
CC human and mouse anti-trkC agonist monoclonal antibodies and antibody
CC fragments of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 1 STSNLAS 7

RESULT 12
AAU74410
ID AAU74410 standard; peptide; 7 AA.
XX
AC AAU74410;

XX 26-MAR-2002 (first entry)
DT
XX
DE Light chain complementarity determining region L2 (CDRL2).
XX
KW Complementarity determining region; CDR; CDRL2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody light chain variable domain.
XX
OS Mus sp.
XX WO200190192-A2.
PN
XX 29-NOV-2001.
PD
XX 24-MAY-2001; 2001WO-US16924.
PF
XX 24-MAY-2000; 2000US-206749P.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20281.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides -
XX
PS Claim 55; Page 57; 64pp; English.
XX
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the light chain variable domain
CC complementarity determining region L2 (CDRL2) incorporated into an
CC antigen-binding protein described in the method of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 1 STSNLAS 7

RESULT 13
AAG80315
ID AAG80315 standard; peptide; 8 AA.
XX
AC AAG80315;
XX

DT 18-FEB-2002 (first entry)
XX
DE Anti-human TNF-alpha CDR-L2 peptide.
XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO200179298-A1.
XX
PD 25-OCT-2001.
XX
PF 18-APR-2001; 2001WO-JP03308.
XX
PR 19-APR-2000; 2000JP-0117394.
XX
PA (SUNR) SUNTORY LTD.
XX
PI Fukuda Y, Nagahira K, Nakanishi T;
XX
DR WPI; 2002-066345/09.
XX
PT Novel heavy and light-chain polypeptides of chimeric and humanised
PT antibodies against human tumour necrosis factor alpha for
PT low-immunogenicity treatment of TNF-related diseases such as toxic
PT shock syndrome -
XX
PS Claim 3b; Page 26; 36pp; Japanese.
XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis
CC factor-alpha (TNF-alpha) light chain CDR1 designated CDR-L2.
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 31; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 2 STSNLAS 8
RESULT 14
AAW89175
ID AAW89175 standard; peptide; 92 AA.
XX
AC AAW89175;
XX
DT 25-MAR-1999 (first entry)
XX
DE Anti-p53 monoclonal antibody 246 variable light chain sequence.
XX
KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 53

FT Misc-difference 86 /note= "unspecified"
FT /note= "unspecified"
FT Misc-difference 90 /note= "unspecified"
FT
XX WO9856416-A1.
PN
XX 17-DEC-1998.
XX
XX 09-JUN-1998; 98WO-IL00266.
PF
XX 09-JUN-1997; 97IL-0121041.
PR
XX (YEDA) YEDA RES & DEV CO LTD.
PA
XX Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
PI Wolkowicz R;
PI
XX WPI; 1999-070296/06.
DR
XX Use of a monoclonal antibody to a tumour-associated antigen - to
PT induce anti-tumour immunity or elicit an increased immune response
PT to the antigen
PT
XX Example 3; Fig 3; 47pp; English.
PS
XX The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarity determining region) on the heavy or light chain of MAB
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of MAB, in a gene delivery vehicle. The present
CC sequence represents the variable light chain sequence from anti-p53 MAB
CC 246. Also described is a method for generating sequence-specific,
CC anti-DNA antibodies (Ab) by immunising a mammal with a MAB directed to a
CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
CC used to treat a wide variety of primary and metastatic cancers,
CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
CC to determine critical sequences in animal or plant breeding); to
CC identify bacteria and other parasites; to determine parentage; in
CC forensic science; to isolate specific genes for DNA vaccination; in gene
CC sequencing and cloning; also possibly for activation of selected
CC therapeutic genes in plants, animals and humans. (A) induce an effective
CC anti-tumour response without causing harm to the patient. The method
CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.
XX
SQ Sequence 92 AA;
Query Match 100.0%; Score 31; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 32 STSNLAS 38
RESULT 15
ABP02151
ID ABP02151 standard; Protein; 93 AA.
XX
AC ABP02151;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:4284.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;

KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

XX Homo sapiens.

OS WO200192523-A2.

PN 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US10836.

PR 30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2002105308/14.

DR N-PSDB; ABN17903.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders

XX Disclosure; SEQ ID 4284; 1037pp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 93 AA;

Query Match 100.0%; Score 31; DB 23; Length 93;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7

Db 15 STSNLAS 21

Search completed: December 23, 2002, 07:25:06
Job time : 4:75775 secs

RESULT 3

SI17623
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17623
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17623
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

|||||

Db 43 STSNLAS 49

RESULT 4

SI17640
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17640
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17640
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

|||||

Db 43 STSNLAS 49

RESULT 5

SI17641
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17641
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17641
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

|||||

Db 43 STSNLAS 49

RESULT 6

SI17642
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17642
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17642
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

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Db 43 STSNLAS 49

RESULT 7

C33730
Ig kappa chain V region (4.68) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C:Accession: C33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: C33730
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
A:Cross-references: GB:M25999; NID:gl97117; PIDN:AAA38915.1; PID:gl97118
A>Note: the authors translated the codon TTG for residue 34 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

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Db 51 STSNLAS 57

RESULT 8

D38601
Ig kappa chain V region (6A7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: D38601
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D38601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-99 <GOS>
A;Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 41 STSNLAS 47

RESULT 9
PH1058
Ig light chain V region (clone 163.72) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1058
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1058
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||
Db 51 STSNLAS 57

RESULT 10
PH1059
Ig light chain V region (clone 17s-cl) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1059
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1059
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
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Db 51 STSNLAS 57

|||||
Db 51 STSNLAS 57

RESULT 11
PH1060
Ig light chain V region (clone 74-cl) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1060
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1060
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||
Db 51 STSNLAS 57

RESULT 12
PT0404
Ig light chain V region (S107/VH11 group 3-23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: PT0404
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodies
A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0404
A;Molecule type: DNA
A;Residues: 1-109 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||
Db 51 STSNLAS 57

RESULT 13
PT0405
Ig light chain V region (S107/VH11 group 3-38) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: PT0405
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodies
A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0405
A;Molecule type: DNA
A;Residues: 1-109 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Job time : 2.38372 secs

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 51 STSNLAS 57
RESULT 14
A32513
Ig kappa chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: A32513
R:Kofler, R.; Strohhal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: A32513
A:Molecule type: DNA
A:Residues: 1-130 <KOF>
A:Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;38-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 73 STSNLAS 79
RESULT 15
PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0013
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0013
A:Molecule type: mRNA
A:Residues: 1-140 <CHE>
A:Experimental source: cell line 4C11
A:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;46-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-118/Region: complementarity-determining 3
F;130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 100.0%; Score 31; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 71 STSNLAS 77

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 0.651163 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	10 US-09-976-787-5	Sequence 5, Appli
2	31	100.0	7	10 US-09-865-198-5	Sequence 5, Appli
3	31	100.0	7	10 US-09-910-059-27	Sequence 27, Appl
4	31	100.0	105	9 US-09-982-107-12	Sequence 12, Appl
5	31	100.0	106	10 US-09-976-787-24	Sequence 24, Appl
6	31	100.0	106	10 US-09-865-198-23	Sequence 23, Appl
7	31	100.0	107	9 US-09-144-886-76	Sequence 76, Appl
8	31	100.0	107	9 US-09-144-886-88	Sequence 88, Appl
9	31	100.0	107	10 US-09-910-059-50	Sequence 50, Appl
10	31	100.0	107	10 US-09-910-059-61	Sequence 61, Appl
11	31	100.0	107	10 US-09-910-059-65	Sequence 65, Appl
12	31	100.0	107	10 US-09-910-059-71	Sequence 71, Appl
13	31	100.0	108	10 US-09-976-787-8	Sequence 8, Appli
14	31	100.0	108	10 US-09-865-198-8	Sequence 9, Appli
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16	31	100.0	112	9 US-09-144-886-89	Sequence 89, Appl
17	31	100.0	235	10 US-09-910-059-17	Sequence 17, Appl
18	31	100.0	235	10 US-09-910-059-52	Sequence 52, Appl
19	31	100.0	235	10 US-09-910-059-97	Sequence 97, Appl

20	31	100.0	235	10	US-09-910-059-99	Sequence 99, Appl
21	31	100.0	238	10	US-09-976-787-29	Sequence 29, Appl
22	31	100.0	238	10	US-09-865-198-28	Sequence 28, Appl
23	31	100.0	240	10	US-09-976-787-28	Sequence 28, Appl
24	31	100.0	240	10	US-09-865-198-27	Sequence 27, Appl
25	31	100.0	669	9	US-09-807-721-2	Sequence 2, Appli
26	28	90.3	7	10	US-09-965-099-13	Sequence 13, Appl
27	28	90.3	7	12	US-10-051-852-13	Sequence 13, Appl
28	28	90.3	8	10	US-09-169-048-16	Sequence 16, Appl
29	28	90.3	8	10	US-09-169-048-28	Sequence 28, Appl
30	28	90.3	27	10	US-09-965-099-55	Sequence 55, Appl
31	28	90.3	27	12	US-10-051-852-55	Sequence 55, Appl
32	28	90.3	93	10	US-09-965-099-35	Sequence 35, Appl
33	28	90.3	93	10	US-09-965-099-66	Sequence 66, Appl
34	28	90.3	93	12	US-10-051-852-35	Sequence 35, Appl
35	28	90.3	93	12	US-10-051-852-66	Sequence 66, Appl
36	28	90.3	106	10	US-09-893-615-89	Sequence 89, Appl
37	28	90.3	106	10	US-09-965-099-105	Sequence 105, App
38	28	90.3	106	12	US-10-051-852-105	Sequence 105, App
39	28	90.3	107	10	US-09-965-099-11	Sequence 11, Appl
40	28	90.3	107	10	US-09-965-099-44	Sequence 44, Appl
41	28	90.3	107	10	US-09-965-099-57	Sequence 57, Appl
42	28	90.3	107	10	US-09-965-099-62	Sequence 62, Appl
43	28	90.3	107	10	US-09-965-099-74	Sequence 74, Appl
44	28	90.3	107	12	US-10-051-852-11	Sequence 11, Appl
45	28	90.3	107	12	US-10-051-852-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-5
; Sequence 5, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-5

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 1 STSNLAS 7
|||||||

RESULT 2
US-09-865-198-5
; Sequence 5, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-5

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 1 STSNLAS 7

RESULT 3

US-09-910-059-27
; Sequence 27, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-27

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 1 STSNLAS 7

RESULT 4

US-09-982-107-12
; Sequence 12, Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12

; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12

Query Match 100.0%; Score 31; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 5

US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match 100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 6

US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 7
US-09-144-886-76
; Sequence 76, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C9 region VL epitope 1
US-09-144-886-76

Query Match 100.0%; Score 31; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 8
US-09-144-886-88
; Sequence 88, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/a clone
; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88

Query Match 100.0%; Score 31; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 9
US-09-910-059-50
; Sequence 50, Application US/09910059
; Patent No. US20020142359A1

; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain variable region
US-09-910-059-50

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 10
US-09-910-059-61
; Sequence 61, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-61

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |

Db 49 STSNLAS 55

RESULT 11

US-09-910-059-65
; Sequence 65, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 65
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-65

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 12

US-09-910-059-71
; Sequence 71, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 71
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-71

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 13

US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match 100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 14

US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match 100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | |
Db 49 STSNLAS 55

RESULT 15

US-09-910-059-9
; Sequence 9, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-9

Query Match 100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|
Db 49 STSNLAS 55

Search completed: December 23, 2002, 07:58:19
Job time : 1.65116 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 1.77907 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	132	2 S05268	Ig kappa chain pre
2	42	87.5	93	2 S17641	Ig kappa chain V r
3	42	87.5	106	2 B54378	Ig light chain V r
4	42	87.5	106	2 PS0070	Ig kappa chain V r
5	40	83.3	35	2 E38601	Ig kappa chain V r
6	40	83.3	99	2 D38601	Ig kappa chain V r
7	38	79.2	91	2 S17626	Ig kappa chain V r
8	38	79.2	117	2 S42466	Ig kappa chain V r
9	38	79.2	140	2 PL0013	Ig kappa chain pre
10	37	77.1	106	2 G27887	Ig kappa chain V r
11	37	77.1	130	2 A32513	Ig kappa chain pre
12	37	77.1	132	2 S40334	Ig kappa chain - h
13	37	77.1	1501	1 B29813	174K ninaC protein
14	36	75.0	86	2 C28195	Ig kappa chain V r
15	36	75.0	886	2 F83862	penicillin-binding
16	35	72.9	91	2 S17628	Ig kappa chain V r
17	35	72.9	107	2 A28195	Ig kappa chain V r
18	35	72.9	108	1 K1HUBN	Ig kappa chain V-I
19	35	72.9	108	2 PL0204	anti-DNA autoantib
20	35	72.9	111	2 S23628	Ig kappa chain V r
21	35	72.9	129	2 S40369	Ig kappa chain - h
22	35	72.9	133	2 S49632	hypothetical prote
23	34	70.8	98	2 S26342	Ig kappa chain V r
24	34	70.8	102	2 S29584	Ig kappa chain V r
25	34	70.8	106	2 PC4282	Ig kappa chain (an
26	34	70.8	108	1 K2DGGM	Ig kappa chain V r
27	34	70.8	108	2 S29581	Ig kappa chain V r
28	34	70.8	128	2 S40379	Ig kappa chain V-J
29	34	70.8	129	2 D32513	Ig kappa chain pre

30 34 70.8 144 2 PL0106 Ig kappa chain pre

31 34 70.8 275 2 H82106 chemotaxis protein

32 34 70.8 341 1 VHBPEL major capsid prote

33 34 70.8 341 2 C90833 major capsid prote

34 34 70.8 341 2 F90900 probable major cap

35 34 70.8 341 2 E85690 probable capsid pr

36 34 70.8 343 1 KHDO cysteine proteinas

37 34 70.8 377 2 T12042 cysteine proteinas

38 34 70.8 380 2 S55923 conserved hypothet

39 34 70.8 397 2 B70048 ABC transporter BH

40 34 70.8 399 2 H84108 probable membrane

41 34 70.8 653 2 S67035 Ig kappa chain V r

42 33 68.8 77 2 D30502 Ig kappa chain V r

43 33 68.8 93 2 S17635 Ig kappa chain V-I

44 33 68.8 108 1 K1HUKU Ig kappa chain V r

45 33 68.8 108 2 PS0069 Ig kappa chain V r

RESULT 1

S05268

Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000

C;Accession: S05268; JL0062; S03846

R;Levy, S.

submitted to the EMBL Data Library, February 1989

A;Reference number: S05267

A;Accession: S05268

A;Molecule type: mRNA

A;Residues: 1-132 <LEV>

A;Cross-references: EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261

R;Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.

J. Exp. Med. 168, 1607-1620, 1988

A;Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An expl

A;Reference number: JL0061; MUID:89035985; PMID:3141553

A;Accession: JL0062

A;Molecule type: mRNA

A;Residues: 1-120 <CAR>

A;Cross-references: EMBL:X14098

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>

F;15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>

F;15-108/Domain: V region (V-kappa-1) <VRE>

F;30-103/Domain: immunoglobulin homology <IMM>

F;109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 100.0%; Score 48; DB 2; Length 132;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 102 QQRSSYPFT 110

RESULT 2

S17641

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S17641

R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A;Title: Making antibody fragments using phage display libraries.

A;Reference number: S17230; MUID:91326098; PMID:1907718

A;Accession: S17641

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-93 <CLA>

ALIGNMENTS

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-83/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 93;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

|||||

Db 82 QQRSSYPFT 90

RESULT 3

B54378

Ig light chain V region anti-triplex DNA - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: B54378

R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence

A;Reference number: A54378; MUID:94165109; PMID:7509814

A;Accession: B54378

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <AGA>

A;Cross-references: GB:S68985; NID:9545746; PIDN:AAB30096.1; PID:9545747

A;Experimental source: spleen and myeloma cell line MOPC 315.43

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 106;

Best Local Similarity 88.9%; Pred. No. 0.29;

Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 QQRSSYPFT 9

|||||

Db 88 QQRSSYPFT 96

RESULT 4

PS0070

Ig kappa chain V region (38C13.V6.1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C;Accession: PS0070

R;Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A;Reference number: A92781; MUID:89310348; PMID:2501443

A;Accession: PS0070

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-106 <LEV>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 106;

Best Local Similarity 88.9%; Pred. No. 0.29;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

|||||

Db 88 QQRSSYPFT 96

RESULT 5

E38601

Ig kappa chain V region (14D2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999

C;Accession: E38601

R;Goshorn, S.C.; Retzel, E.; Jermerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same anti

A;Reference number: A38601; MUID:91115823; PMID:1703527

A;Accession: E38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-35 <GOS>

A;Cross-references: GB:M57982; NID:gl96410; PIDN:AAA63363.1; PID:gl96411

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 83.3%; Score 40; DB 2; Length 35;

Best Local Similarity 87.5%; Pred. No. 0.26;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9

|||||

Db 24 QRSSYPFT 31

RESULT 6

D38601

Ig kappa chain V region (6A7) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000

C;Accession: D38601

R;Goshorn, S.C.; Retzel, E.; Jermerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same anti

A;Reference number: A38601; MUID:91115823; PMID:1703527

A;Accession: D38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-99 <GOS>

A;Cross-references: GB:M57981; NID:gl96408; PIDN:AAA63362.1; PID:gl96409

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 40; DB 2; Length 99;

Best Local Similarity 77.8%; Pred. No. 0.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

|||||

Db 80 QHRSSYPFT 88

RESULT 7

S17626

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S17626

R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A;Title: Making antibody fragments using phage display libraries.

A;Reference number: S17230; MUID:91326098; PMID:1907718

A;Accession: S17626

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-91 <CLA>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 91;

Best Local Similarity 88.9%; Pred. No. 1.6;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
| | | | | | | |
Db 80 QQRSSYPPT 88

RESULT 8
S42466
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
R;Shiyanov, P.A.; Bernalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42466
A;Accession: S42466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <SHI>
A;Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | |
Db 99 QQYSSYPYT 107

RESULT 9
PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0013
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0013
A;Molecule type: mRNA
A;Residues: 1-140 <CHE>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;46-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-118/Region: complementarity-determining 3
F;130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 79.2%; Score 38; DB 2; Length 140;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | |
Db 110 QQRSSYPPT 118

RESULT 10
G27887
Ig kappa chain V region (H18-S415) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000

C;Accession: G27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: G27887
A;Molecule type: DNA
A;Residues: 1-106 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 106;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QQRSSYPFT 9
| | | | | | | |
Db 89 QQRSSYPPT 96

RESULT 11
A32513
Ig kappa chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: A32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization a
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: A32513
A;Molecule type: DNA
A;Residues: 1-130 <KOF>
A;Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-113/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 130;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
| | | | | | | |
Db 112 QQYSGYPFT 120

RESULT 12
S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSSYPFT 9
||:|||||
Db 110 QQFNSYPFT 118

RESULT 13
B29813
174K ninaC protein - fruit fly (Drosophila melanogaster)
N:Contains: protein kinase (EC 2.7.1.-)
C:Species: Drosophila melanogaster
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: B29813
R;Montell, C.; Rubin, G.M.
Cell 52, 757-772, 1988
A;Title: The Drosophila ninaC locus encodes two photoreceptor cell specific proteins with
A;Reference number: A90898; MUID:88151067; PMID:2449973
A;Accession: B29813
A;Molecule type: mRNA
A;Residues: 1-1501 <MON>
A;Cross-references: GB:M20230; NID:g157967; PIDN:AAA28721.1; PID:g157968
C;Genetics:
A;Gene: FlyBase:ninaC
A;Cross-references: FlyBase:FBgn0002938
C;Superfamily: ninaC protein; myosin motor domain homology; protein kinase homology
C;Keywords: actin binding; alternative splicing; ATP; nucleotide binding; P-loop; phosph
F;14-282/Domain: protein kinase homology <KIN>
F;335-1022/Domain: myosin motor domain homology <MMOT>
F;425-432/Region: nucleotide-binding motif A (P-loop)
F;911-936/Region: actin binding #status predicted
F;1054-1501/Domain: carboxyl-terminal <CBT>
F;45,60,145/Active site: Lys, Glu, Asp #status predicted
F;431/Binding site: ATP (Lys) #status predicted

Query Match 77.1%; Score 37; DB 1; Length 1501;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYP 7
||| |||
Db 1352 QQRSSYP 1358

RESULT 14
C28195
Ig kappa chain V region (anti-haloperidol antibody C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-May-1997
C;Accession: C28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: C28195
A;Molecule type: mRNA
A;Residues: 1-86 <SHE>
A;Cross-references: GB:M19768
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 75.0%; Score 36; DB 2; Length 86;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
||:|||||
Db 68 QQXNSYPFT 76

RESULT 15
F83862
penicillin-binding proteins 1A/1B ponA [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83862
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83862
A;Status: preliminary -
A;Molecule type: DNA
A;Residues: 1-886 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA05421.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: ponA

Query Match 75.0%; Score 36; DB 2; Length 886;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 8
||:|||||
Db 282 QERESYPFT 289

Search completed: December 23, 2002, 07:31:37
Job time : 2.77907 secs